Sequence Protocol

- (1) GENERAL INFORMATION:
 - (i) APPLICANT:
 - (A) NAME: metaGen Gesellschaft für Genomforschung mbH
 - (B) STREET: Ihnestrasse 63
 - (C) CITY: Berlin
 - (E) COUNTRY: Germany
 - (F) POSTAL CODE (ZIP): D-14195
 - (G) TELEPHONE: (030)-8413 1673
 - (H) FAX: (030)-8413 1674
 - (ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Pancreas Tumor Tissue
 - (iii) Number of sequences: 633
 - (iv) COMPUTER-READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)
- (2) INFORMATION ON SEQ ID NO. 1:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1202 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

cttcatcgat agetaccget gettecaace aaageaggag ggggeettea eetgetggte 60 agcagtcact ggcgcccgcc atctcaacta tggctcccgg cttgactata ccctggggga 120 caggaccetg gtcatagaca cettteagge etetteetg etgeetgagg tgatgggete 180 tgaccactgc cctgtgggtg cagtcttgag tgtgtcctct gtgcctgcaa aacagtgccc 240 acctetgtge accegettee teeetgagtt tgeaggeace cageteaaga teettegett 300 cctagttcct ctcgaacaaa gtcctgtgtt ggagcagtcg acgctgcagc acaacaatca 360 aaccegggta cagacatgee aaaacaaage ccaagtgege tcaaccagge etcageecag 420 tcaggttggc tctagcagag gccagaaaaa cctgaagagc tactttcagc cctcccctag 480 ctgtccccaa gcctctcctg acatagaget gcctagecta ccactgatga gcgccctcat 540 gaccccgaag actccagaag agaaggcagt ggccaaagtg gtgaaggggc aggccaagac 600 ttcagaagcc aaagatgaga aggagttacg gacctcattc tggaagtctg tgctggcggg 660 gecettgege acaecectet gtgggggeea eagggageea tgtgtgatge gtaetgtgaa 720 gaagecagga eccaacttgg geegeégett etacatgtgt geeaggeece ggggteetee 780 cactgacccc tecteceggt geaattette etetggagea ggeecagetg aaccaatgga 840 ggcctgggga catctggcat ggtcacccct gcacatgatc tgaggccagc tccccttccc 900 tgagetgeet cetgettete ceteaaagte tectaceett etetteetet tttaageeet 960 ctcttcctcg ctttccttcc tacctagete cttgttggtg agettcttgt gccttaatcc1020 tgtgacccag ccccttacac cactttccac cttcctgtcc gaagtacacg gacactagct1080 gccccaggaa gttgtgtgat tttaaatcac ttctgtcttt gctggaaagt gtatttgtgc1140 ataaataaag totgtgtatt tgtttcaaaa aaaaaaaaaa aaaaaaagga ggtttgaagg1200 gg

(2) INFORMATION ON SEQ ID NO. 2:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1072 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

cctccatcag ctcgccgcgc agcggctgta tttgcggcct gtgcgagtag gcgcttgggc actcaqtete ectggegage gaegggeaga aatetegaae eagtggageg caetegtaae 120 ctggatccca gaaggtcgcg aaggcagtac cgtttcctca gcggcggact gctgcagtaa 180 gaatgtettt tecaecteat ttgaategee eteceatggg aateceagea eteceaceag 240 ggatcccacc cccgcagttt ccaggatttc ctccacctgt acctccaggg accccaatga 300 ttootgtacc aatgagcatt atggctcotg ctccaactgt cttagtaccc actgtgtcta 360 tqqttqqaaa qcatttgggc gcaagaaagg atcatccagg cttaaaggct aaagaaaatg 420 atgaaaattg tggtcctact accactgttt ttgttggcaa catttccgag aaagcttcag 480 acatqcttat aagacaactc ttagctaaat gtggtttggt tttgagctgg aagagagtac 540 aaggtgcttc cggaaagctt caagccttcg gattctgtga gtacaaggag ccagaatcta 600 ccctccqtqc actcagatta ttacatgacc tqcaaattqg agagaaaaag ctactcgtta 660 aagttgatgc aaagacaaag gcacagctgg atgaatggaa agcaaagaag aaagcttcta 720 atgggaatgc aaggccagaa actgtcacta atgacgatga agaagccttg gatgaagaaa 780 caaagaggag agatcagatg attaaagggg ctattgaagt tttaattcgt gaatactcca 840. gtgagctaaa tgccccctca caggaatctg attctcaccc ccaggaagaa gaagaaggaa 900 aagaaggagg acattttccg cagatttcca gtggccccac tgatccctta tccactcatc 960 actaaggagg atataaatgc tatagaaatg gaagaagaca aaagagacct gatatctcga1020 gagatcagca aattcagaga cacacataag aaactggaag aagagaaagg ca

- (2) INFORMATION ON SEQ ID NO. 3:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1468 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
gcacgaggta ttatgctgtc gtatggctcc actgcagaaa gcaaaagtaa taagactaat
aaaaatatca cctgagaaac ctataacatt ggctgttggt gatggtgcta atgacgtaag 120
catgatacag gaggeecatg ttggeatagg aateatgggt aaagaaggaa gacaggetge 180
aagaaacagt gactatgcaa tagccagatt taagttcctc tccaaattgc tttttgttca 240
tggtcatttt tattatatta gaatagctac ccttgtacag tattttttt ataagaatgt 300
gtgctttatc acaccccagt ttttatatca gttctactgt ttgttttctc agcaaacatt 360
gtatgacage gtgtacetga etttatacaa tatttgtttt aetteeetae etattetgat 420
atatagtett ttggaacage atgtagacee teatgtgtta caaaataage ceaceettta 480
tegagaeatt agtaaaaace geetettaag tattaaaaca tttetttatt ggaceateet 540
gggcttcagt catgccttta ttttcttttt tggatcctat ttactaatag ggaaagatac 600
atctctgctt ggaaatggcc agatgtttgg aaactggaca tttggcactt tggtcttcac 660
agtcatggtt attacagtca caataaagat ggctctggaa actcattttt ggacttggat 720
agggattete tggccatttt tgggctecca gaatatgtat tttgtgttta tteageteet 840
gtcaagtggt tctgcttggt ttgccataat cctcatggtt gttacatgtc tatttcttga 900
tatcataaag aaggtetttg accgacacet ceacectaca agtactgaaa aggeacagat 960
gtactccaac acagttgctt taagtgacga gttcatcgca ctgcagccat tgtcgagggc1020
aaggaatcag ctgagcaaac ttagcttact gaaacaaatg caggtatcaa gtgcttggac1080
tccatgtgct gtttcccgga aggagaagca gcgtgtgcat ctgttggaag aatgctggaa1140
cgagttatag gaagatgtag tccaacccac atcagcaggt gtgaaatctc tctaagtagc1200
ctttgctgca gatgagtatc ctatctggaa caggatgaac ctgccgctct agatacctaa1260
taaatcagca gctggtttta ccaactgaag caggaagtct gctatttatt agcactcttt1320
ggtggtagat ttcactttgt ggctttgggg taagggcttt ttcactcaca aaggaagaga1380
aagcaccttt gaagagactt catctaatga acaaaaaatt ttgtttcata atctttctaa1440
aatgggctca gtaggagtgg gtgtatgg
```

- (2) INFORMATION ON SEQ ID NO. 4:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2331 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
eggetegaga aaggaeetet ecetttteag atgeetggea tgaggettee agaaacceag
gttcttccag gagaaataga tgagactcct ctttccaagc caggacatga ccttgccagc 120
atggaggata aaacagagaa atggtcttcc cagcctgaag gtccacttaa attgaaagct 180
tcaagtactg atatgccatc ccagatttct gtggttaatg tggatcaact gtgggaagat 240
totgtoctaa otgtoaaatt occoaaatta atggtaccaa ggttotoott occtgoocco 300
ageteagagg atgatgtgtt catececact gtgagggaag tgeagtgtee agaggeeaat 360
attgatacag ccctttgtaa ggaaagtccg gggctctggg gagccagcat cctgaaggca 420
ggtgctgggg tccctgggga gcagcctgtg gaccttaacc tgcctttgga agctcccca 480
atttcaaagg tcagagtgca tattcagggt gctcaggttg aaagtcaaga ggtcactata 540
cacagcatag tgacaccaga gtttgtagat ctctcagtac ccaggacttt ttccactcag 600
attgtgcggg aatcagagat ccccacgtca gagattcaaa caccttcgta cggattttcc 660
ttattaaaag tgaaaatccc agagccccac acgcaggdta gagtgtacad aacaatgact 720
caacactcta ggactcagga gggcacagaa gaggctccca tacaagccac cccaggagta 780
gactccattt ctggagatct ccagcctgac actggagaac catttgagat gatctcttcc 840
agogtoaatg tactgggaca gcaaacactc acatttgaag ttoottotgg ccaccagett 900
gcagacaget gttcagatga ggagccagca gaaattettg agttteecce tgatgatage 960
caagaggcaa ccacaccact ggcagatgaa ggcagggctc caaaagacaa accagaaagt1020
aaaaaatctg gtctgctctg gttttggctt ccaaacattg ggttttcctc ttctgttgat1080
gagacaggtg ttgattccaa aaatgacgtc cagagatctg ctcccattca aacacagcct1140
gaggcacgac cagaggcaga actgcctaaa aaacaggaga aggcaggctg gttccgattt1200
cccaaattag ggttctcctc atctcctacc aagaaaagca aaagcaccga agatggggcal260
gagctggaag aacaaaact tcaagaagaa acaatcacgt tttttgatgc ccgagaaagt1320
tteteecetg aagagaagga agagggtgaa etgateggge etgtgggeae tgggetggae1380
tccagagtga tggtgacatc cgcggcaaga acagagttaa tcctgcccga gcaggacaga1440
aaagctgacg atgaaagcaa agggtcaggc ctgggaccaa atgaaggctg agaggtatgg1500
ctcatcagta caagagagat gcaaaaaact aagttggaaa gtaaaggcta cacacacata1560
tggagcaccc catcccacag cacattacat ccacctcact tcacagaacg gagaacagag1620
cagaaatgac cagaacacct ttgtcaccat cacacagccc tcctaaaatg gaaccaaagc1680
ttcccagete ceteaaaget ttggatgeaa agaaggeace etgaetteea caagacacea1740
gaattcacac ggtactcaga ggcactgctg gggaagtttg ttggtcttta ttagataaat1800
ttccagagac ctgtccataa tacccaacag aacatgactg tttctttgag gaaagggtta1860
taatgtetgt ggtgtacaag tegtttttgg tataaettet tteetgetge tgetgettee1920
cggcaaacat agttttccta tttcaggcag agtgcggtat attccaggaa acactgtttc1980
ctactcactt agcttacttc tttgttgaat gcctcactaa tggcaagttt caagatgttt2040
tgggtgacaa tgcacacatg ctgggcaaaa gggtgatggc cagtggctgg cagctgggcc2100
agcagaaget aggacatetg tgagttgtca tteteateta tecatgteea etggeetgee2160
agcateegee agtgeettge cagtgtgeae ggteecacae tgtggeecet gagteeceta2220
atgtacacge tgcagecaga atgcagatgg agetggettg getgtteeet ggatgggcaa2280
taaagaaagt gctgcatccc aaaaaaaaa aaaaagtaaa aaaaaaagg g
```

(2) INFORMATION ON SEQ ID NO. 5:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1925 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
aataaaaaaa attgtattta cttagaagca ttcagaatgt caacaaaaca gccgcaattt
tttttttgca attacagagt ggtattcagt taacagaaca acaattatct tcgtataagc 120
tgcatcagag acaactgaag atgaaaaaaa taaaacccaa aaagaaaacc aaaagaaaaa 180
aaaaaaaaaa acaaaaaaca aaactaccat ccccatatat aactaatttg tgctgtgcac 240
caacaagaac ctgctttaaa tttccatgcc aatttacaac ccccatactg taccaggcaa 300
ggttagtggc tattgaaaat accaccagga cagggctatc taaagacaca ttcggtagtg 360
tgttaactat acaaaaaaag acactgtaca gtttaaaaac aaatcttaca cagccttaca 420
tttcaatttt tttctttaaa aggagtgagt tgtgtacagg ggggttaaat gctttataga 480
caagaaaaaa aaaactgcgc tagaaccaac ttattcatca tcatcatctt cttcttcatc 540
tteatettet teatetteet eeteeteete ateetettea tetteeteat etteeteete 600
ttccttcttt ttcttgcttt tttcagcctt gacaactccc ttttttgctg catcaggctt 660
teetttaget egatatgeag caatateett ttegtatttt teetteaett egeageette 720
ttttcataag gctgcttgtc atctgcagca gtgttattcc acatctctcc cagtttcttc 780
qcaacatcac caatggacag gccaggatgt tctcctttga tttttgggcg atactcagag 840
caqaaqaqqa agaaggccqa aggaggcctc ttgggtgcat tgggatcctt gaacttcttt 900
tttgtctccc ctttgggagg gatataggtt ttcatttctc tttcataacg ggccttgtcc 960
qcttttgcca tatcttcaaa ttttcctttc tctttagcag acatggtctt ccacctctct1020
gageacttet tagaaaacte tgagaagttg actgaageat etgggtgett ettettatge1080
tectecegae aagtttgeae aaaaaatgea tatgatgaea ttttgeetet eggettettal140
ggatctcctt tgcccatgtt tagttatttt tctaaaaaat aaaataaata tttgatgtta1200
gcaataaaat tatgacatat aagaccttaa agtacttagt aagggaatga aaaccaaagt1260
actggttatt taacacagta gcgacatcaa cctccgtaaa atcagacaag aatatggccg1320
tcagggcgat ctcaaaaagt ctagacacaa agatataccc atacagtatt ccctatctat1440
ccgcccgagt ctgctctgaa tgagtatcta actggtcact taaacgattt taaaatctag1500
aacaccattt taaaccaacc aaaccaaagg tcagaaaaca tgctgccaat tcgtggcttt1560
gcactagata gggaataaac aagggcctaa gcgagtcgac tcttcctaat tatgggacct1620
taaaaaaaaa aatcaccgtg caccgaaagt ttcaaaaaac accctctttg cataaaactt1680
tgctccaaaq aqqqaqcaqc aqccaqctcc ggtgctcgga acccggttgg gaggtgcggt1740.
gccaccgcga ggcagcctcg tttcctatcg gtttggccct gagatgtatt tctgttctga1800
ctaaacacgt ccggtctgaa gtttctccga gtaaacaagg atgagggaca aaagccactc1860
ctgctcgtgg ctcggtggcc ccctcccca actcgggaag tattttttgg agccgtcaaa1920
gttgg
```

- (2) INFORMATION ON SEQ ID NO. 6:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1368 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
qtcqqqqaqc qcqgqqccqq qqcccaqqqq accccqqqcc acqqaqaqcq qqaaqaqqat 60
ggattgcccg gccctccccc ccggatggaa gaaggaggaa gtgatccgaa aatctgggct 120
aagtgctggc aagagcgatg tctactactt cagtccaagt ggtaagaagt tcagaagcaa 180
gcctcagttg gcaaggtacc tgggaaatac tgttgatctc agcagttttg acttcagaac 240
tggaaagatg atgcctagta aattacagaa gaacaaacag agactgcgaa acgatcctct 300
caatcaaaat aagggtaaac cagacttgaa tacaacattg ccaattagac aaacagcatc 360
aattttcaaa caaccggtaa ccaaagtcac aaatcatcct agtaataaag tgaaatcaga 420
cccacacga atgaatgaac agccacgtca gcttttctgg gagaagaggc tacaaggact 480
tagtgcatca gatgtaacag aacaaattat aaaaaccatg gaactaccca aaggtcttca 540
aggagttggt ccaggtagca atgatgagac ccttttatct gctgttgcca gtgctttgca 600
cacaagetet gegecaatea cagggeaagt eteegetget gtggaaaaga accetgetgt 660
ttggcttaac acatctcaac ccctctgcaa agcttttatt gtcacagatg aagacatcag 720
gaaacaggaa gagcgagtac agcaagtacg caagaaattg gaagaagcac tgatggcaga 780
catcttgtcg cgagctgctg atacagaaga gatggatatt gaaatggaca gtggagatga 840
agoctaagaa tatgatcagg taactttcga ccgactttcc ccaagagaaa attcctagaa 900
attgaacaaa aatgtttcca ctggcttttg cctgtaagaa aaaaaatgta cccgagcaca 960
tagagetttt taatageact aaccaatgee tttttagatg tatttttgat gtatatatet1020
attattcaaa aaatcatgtt tattttgagt cctaggactt aaaattagtc ttttgtaata1080
tcaagcagga ccctaagatg aagctgagct tttgatgcca ggtgcaatct actggaaatg1140
tagcacttac gtaaaacatt tgtttccccc acagttttaa taagaacaga tcaggaattc1200
taaataaatt tcccagttaa agattattgt gacttcactg tatataaaca tatttttata1260
ctttattgaa aggggacacc tgtacattct tccatcatca ctgtaaagac aaataaatga1320
ttatattcac aaaaaaaaa aaaacaccgg gggggggccc gggcccca
```

- (2) INFORMATION ON SEQ ID NO. 7:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

gaatgeeett tgggggeeag gggeeeetgg gageeeegee accettteee acttggeegg 60 ggtgeeegea geegeeacee etgeaegeat ggeaggetgg caceeecea gageeeteee120 cacageeage ageetteea cagteactge eetteeegea gteeeeagee tteeetaegg180 ceteaecege acceeeteag ageeeaggge tgeaaeceet cattateeae cacgeaeaga240 tggtacaget ggggetgaae aaccacatgt ggaaceagag agggteeeag gegeeegagg300 acaagaegea ggaggeagaa tgacegettg teettgeetg accagetggg gaacaaceet360 ggaeegagge ateggeeagg acceatagag caceeggttt tteeetgtge cettttggaa420 attg

- (2) INFORMATION ON SEQ ID NO. 8:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1020 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO.
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```
caagtaaatg cagcactagt gggtgggatt gaggctatgc cctggtgcat aaatagagac 60
teagetgtge tggcacacte ageggetetg gacegeatee tageegeega eteacacaag 120
qcaggtqggt gaggaaatcc agagttgcca tggagaaaat tccagtgtca gcattcttgc 180
teettgtgge ceteteetae actetggeea gagataeeae agteaaacet ggageeaaaa 240
aggacacaaa ggactetega eecaaaetge eecagaeeet eteeagaggt tggggtgaee 300
aactcatctg gactcagaca tatgaagaag ctctatataa atccaagaca agcaacaaac 360
ccttgatgat tattcatcac ttggatgagt gcccacacag tcaagcttta aagaaagtgt 420
ttgctgaaaa taaagaaatc cagaaattgg cagagcagtt tgtcctcctc aatctggttt 480
atgaaacaac tgacaaacac ctttctcctg atggccagta tgtccccagg attatgtttg 540
ttgacccatc tctgacagtt agagccgata tcactggaag atattcaaac cgtctctatg 600
cttacgaacc tgcagataca gctctgttgc ttgacaacat gaagaaagct ctcaagttgc 660
tqaaqactga attgtaaaga aaaaaaatct ccaagccctt ctgtctgtca ggccttgaga 720
cttgaaacca gaagaagtgt gagaagactg gctagtgtgg aagcatagtg aacacactga 780
ttaggttatg gtttaatgtt acaacaacta ttttttaaga aaaacaagtt ttagaaattt 840
qqtttcaagt gtacatgtgt gaaaacaata ttgtatacta ccatagtgag ccatgatttt 900
ctaaaaaaaa aaataaatgt tttgggggtg ttctgttttc tccaaaaaaa aaaaaaaaa 960
aaaaaaaaaa aaaaaaaaaa aaaaattgcc cccaagggga cgggttacaa ttgggggggg1020
```

- (2) INFORMATION ON SEQ ID NO. 9:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 718 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

tgaaaaagta aactacattt cctagcgtge ccgtgtcttg cttccggctg acgtgtcttt 60 caggaagagg agctggtgag aagacagcga aatggcgcct ccggcccccg gcccggcctc120 cggcggctcc ggggaggtag acgagctgtt cgacgtaaag aacgccttct acatcggcag180 ctaccagcag tgcataaacg aggcgcacgg gtgaagctgt caagcccaga gagaagcgtg240 gagaggtaca accctcctc gcccctgag ctccaggccg tgcgcatgtt tgctgactac360 ctcgcccacg agagtcggag ggacagcatc gtggccgagc tggaccgaga gatgagcag420 agcgtggacg tgaccaacac caccttcctg ctcatggccg tcccatcta tctccacgac480 cagaacccgg atgccgcct gcgtgcgctg caccaggggg acagcctga gtgcacagc540 atgaccagtg agatcctct gaagctgac ctcacccagc tcgaccggaa ggagctgaag600 agaatgcagg acctggacg ggatccccc gcgtccccc ctcacccagc tcaaggtct ggtaagcttg660 caacgggtgt aaaaagctcaa ggatcctct gattcaggg attggtaaaa ttgttcca 718

(2) INFORMATION ON SEQ ID NO. 10:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1202 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

geaggacegt cattgacgee atgagegege tgetgegget getgegeacg ggtgeeceag 60 ccgctgcgtg cctgcggttg gggaccagtg cagggaccgg gtcgcgccgt gctatggccc 120 tgtaccacac tgaggagcgc ggccagccct gctcgcagaa ttaccgcctc ttctttaaga 180 atgtaactgg tcactacatt tccccctttc atgatattcc tctgaaggtg aactctaaag 240 aggaaaatgg cattcctatg aagaaagcac gaaatgatga atatgagaat ctgtttaata 300 tgattgtaga aatacctcgg tggacaaatg ctaaaatgga gattgccacc aaggagccaa 360 tgaatcccat taaacaatat gtaaaggatg gaaagctacg ctatgtggcg aatatcttcc 420 cttacaaggg ttatatatgg aattatggta ccctccctca gacttgggaa gatccccatg 480 aaaaagataa gagcacgaac tgctttggag ataatgatcc tattgatgtt tgcgaaatag 540 gctcaaagat tctttcttgt ggagaagtta ttcatgtgaa gatccttgga attttggctc 600 ttattgatga aggtgaaaca gattggaaat taattgctat caatgcgaat gatcctgaag 660 cctcaaagtt tcatgatatt gatgatgtta agaagttcaa accgggttac ctggaagcta 720 ctcttaattg gtttagatta tataaggtac cagatggaaa accagaaaac cagtttgctt 780 ttaatggaga attcaaaaac aaggcttttg ctcttgaagt tattaaatcc actcatcaat 840 gttggaaagc attgcttatg aagaagtgta atggaggagc tataaattgc acaaacgtgc 900 agatatetga tagecettte egttgeacte aagaggaage aagateatta gttgaategg 960 tatcatcttc accaaataaa gaaagtaatg aagaagagca agtgtggcac ttccttggca1020 agtgattgaa acatctgaaa ttctgctgtc aagattccca tctctaagga ctccaagtgc1080 tagagacaag ggggtctatg agcatttact gacttcctgt taaaacttca ttttttcaaa1140 1202 aa

(2) INFORMATION ON SEQ ID NO. 11:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1610 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
ggagccggga ctcgcgggcg gcggcgggg gcgtcgctgc gcggctggcc ggtgaggccg
cggcatgggg cgagtgcagc tcttcgagat cagcctgagc cacggccgcg tcgtctacag 120
ccccggggag ccgttggctg ggaccgtgcg cgtgcgcctg ggggcaccgc tgccgttccg 180
agccatccgg gtgacctgca taggttcctg cggggtctcc aacaaggcta atgacacage 240
gtgggtagtg gaggagggtt acttcaacag ttccctgtcg ctggcagaca aggggagcct 300
qcccqctgga gagcacagct tccccttcca gttcctgctt cctgccactg cacccacgtc 360
ctttgagggt cctttcggga agatcgtgca ccaggtgagg gccgccatcc acacgccacg 420
gttttccaag gatcacaagt gcagcctcgt gttctatatc ttgagcccct tgaacctgaa 480
cagcatecca qacattgage aacceaacgt ggeetetgee accaagaagt teteetacaa 540
qctqqtqaaq acgggcagcg tggtcctcac agccagcact gatctccgcg gctatgtggt 600
ggggcaggca ctgcagctgc atgccgacgt tgagaaccag tcaggcaagg acaccagccc 660
tgtggtggcc agtctgctgc agaaagtgtc ctataaggcc aagcgctgga tccacgacgt 720
acggaccatt gcggaggtgg agggtgcggg cgtcaaggcc tggcggcggg cgcagtggca 780
cgagcagatc ctggtgcctg ccttgcccca gtcggccctg ccgggctgca gcctcatcca 840
catcgactac tacttacagg tctctctgaa ggcgccggaa gctactgtga ccctcccggt 900
cttcattggc aatattgctg tgaaccatgc cccagtgagc ccccggccag gcctggggct 960
gcctcctggg gccccacccc tggtggtgcc ttccgcacca ccccaggagg aggctgaggc1020
tgaggetgeg getggeggee eccaettett ggaceeegte tteeteteea ecaagageea1080
ttcgcagcgg cagcccctgc tggccacctt gagttctgtg cctggtgcgc cggagccctg1140
ccctcaggat ggcagccctg cctcacaccc gctgcaccct cccttgtgca tttcaacagg1200
tgccactgtc ccctactttg cagagggctc cggggggcca gtgcccacta ccagcacctt1260
gattetteet ecagagtaca gttettgggg etacecetat gaggeeceae egtettatgal320
qcagagctgc ggcggcgtgg aacccagcct gacccctgag agctgacccc gtgctgcctt1380
ctccaggcag gcctggcctc tgccctggga ctgggggcc cagggcctcg tgccttctct1440
cttggcctag cctggcccac tcaggacctg cccagcctct gccagctcct ctgcatccgc1500
cctcttctcc ctggggctgg ggtgggggtg gcagggagct gggacctgga gagacaactc1560
```

(2) INFORMATION ON SEQ ID NO. 12:

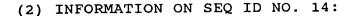
- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2155 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

							60
,	cacgcaagga	tgaggcgggg	tttcgccgtg	gcgcgcatgc	gtgcagcaaa	gaatggagga	60
	at cadaaccc	gaacggaagc	gggctcgcac	cgacgaggtg	cergeeggag	gaageegeee	120
	caaaacaaaa	gatgaggacg	acgaggacta	cgtgccctat	gracegreac	ggcagcgccg	100
	acaactacta	ctccagaage	tactacaaca	aagacgcaag	ggagetgegg	aggaagagca	240
	acaddacado	ggtagtgaac	cccqqqqaqa	tgaggacgac	atteetgetag	gccccagcc	300
	caacgtcage	ctcctggatc	agcaccagca	ccttaaagag	aaggetgaag	cycycaaaga	360
	atctaccaaa	gagaagcagc	tqaaggaaga	agagaagatc	ctggagagtg	Ligiting	120
	cogaggattg	atgtcagtga	aggagatggc	taagggcatt	acgtatgatg	accccatcaa	480
	aaccadctdd	actccacccc	gttatgttct	gagcatgtct	gaagagcgac	argagegege	540
	acagaagaaa	taccacatcc	tggtggaggg	agacggtatc	ccaccaccca	ccaagageee	600
	caaggaaatg	aagtttcctg	cagccatcct	gagaggcctg	aagaagaaag	gcattcacca	660
		atteagatee	agggcatccc	caccattcta	totggccgrg	acatgatagg	720
	categettte	acgggttcag	gcaagacact	ggtgttcacg	ttgcccgtca	ccatgitting	700
	actacaacaa	gagaagaggt	tacccttctc	aaagcgcgag	gggcccctatg	gactcaccat	040
	at accept ca	caggagetag	cccaacaaac	ccatggcatc	ctggagtact	actigotigotic	300
	-c+cc3cc3c	gacageteae	cactcctgcg	Ctdcdccctc	tgcattgggg	gcatgcccgc	200
	daaadadcad	atggagacca	tccgacacgg	tgtacacatg	atggtggcca	, ccccggggcg.	1020
	catastaget	ttactacaga	agaagatggt	caqcctagac	accegace	acceggeeee.	1000
	ggacgaggct	gaccgcatga	tcgacatggg	cttcgagggt	gacatecgia	CCatcttctc	1140
	ctacttcaad	ddccadcdac	agaccctgct	cttcagtgcc	accatgeega	agaagaccca	1200
	as act t t act	aadadt.dccc	ttgtaaagcc	tgtgaccatc	aatgtggggc	gegergggge	1200
	taccaaccta	gatgtcatcc	aggaggtaga	atatgtgaag	gaggaggcca	agatygtgta	132,0
	cctactcaaa	tacctacaga	agacaccccc	gcctgtactc	atctttgcag	agaayaaygc	1300
	agacgtggac	gccatccacg	agtacctgct	gctcaagggg	gttgaggccg	Lagiciatica	T440
		gaccaggagg	aacggactaa	ggccatcgag	gcattccggg	agggcaagaa	1300
	gastatacts	gtagggagag	acgttgcctc	caagggcctg	gacttccctg	ccatccagca	1200
	cotcatcaat	tatgacatgo	cagaggagat	tgagaactat	gtacaccgga	ttggccgcac	1620
	cagacactca	ggaaacacag	gcatcgccac	taccttcatc	aacaaagcyt	gryargagic	1000
		gacctcaaag	cactactact	agaagccaag	cagaaggtgc	cgcccgtgct	1/40
		cattgcgggg	atgagtccat	gctggacatt	ggaggagagc	gcggctgtgc	1800
	cttctacaaa	aacctaaatc	atcggatcac	tgactgcccc	: aaactcgagg	ctatgcagac	1860
	caadcaddto	agcaacatco	gtcgcaagga	ctacctggco	: cacagctcca	tggacttctg	17920
	agccgacagt	cttcccttct	ctccaagagg	cctcagtccc	: caagactgcc	accaytotac	.1900
	acatacadca	acccctaga	cagaatcagc	atttcagctc	: agetggeetg	gaatgggtta	2040
	gactagtect	aactacctat	: tccctgtgct	cttcagaatt	. actgulling	CCCCCCCC	22100
	ccccagctgc	cattaaagco	: caaacctcta	gcccaaaaaa	aaaaaaaaa	aaaaa	2155
		. -					

- (2) INFORMATION ON SEQ ID NO. 13:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1743 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```
cctqqqcqqq ccctqcqtca ggttqcaqtt tcacttttaq ctctqqqcac ctccaqctcc
tgctcqccqq acggctccca gggagagcag acgcgccaqa cgcgccaccc tcggggcgcc 120
gacqqtcacq qaqcatqqqq tcqqcctttq aqcqqqtaqt ccqqaqaqtq qtccaqqaqc 180
 tggaccatgg tggggagttc atccctgtga ccagcctgca gagctccact ggcttccagc 240
 cctactgcct ggtggttagg aagccctcaa gctcatggtt ctggaaaccc cgttataagt 300
qtqtcaacct qtctatcaag gacatcctgg agccggatgc cgcggaacca gacgtgcaqc 360
gtggcaggag cttccacttc tacgatgcca tggatgggca gatacagggc agcgtggagc 420
 tggcagcccc aggacaggca aagategcag geggggeege ggtgtetgae agetecagea 480.
 cctcaatgaa tgtgtactcg ctgagtgtgg accctaacac ctggcagact ctgctccatg 540-...
 agaggcacct geggeageca gaacacaaag teetgeagea getgegeage geggggacaa 600
 cgtgtacgtg gtgactgagg tgctgcagac acagaaggag gtggaagtca cgcgcaccca 660
 caagegggag ggetegggee ggtttteeet geeeggagee aegtgettge agggtgaggg 720
 ccagggccat ctgagccaga agaagacggt caccatcccc tcaggcagca ccctcgcatt 780
 ccgggtggcc cagctggtta ttgactctga cttggacgtc cttctcttcc cggataagaa 840
 gcagaggacc ttccagccac ccgcgacagg ccacaagcgt tccacgagcg aaggcgcctg 900
 gccacagctg ccctctggcc tctccatgat gaggtgcctc cacaacttcc tgacagatgg 960
 qqtccctqcq qaqqqqqqt tcactqaaqa cttccaqqqc ctacqqqcaq aqqtqqaqac1020
 catctccaag gaactggage ttttggacag agagetgtge cagetgetge tggagggeet1080
 ggagggggtg ctgcgggacc agctggccct gcgagccttg gaggaggcgc tggagcaggg1140
 ccagageett gggeeggtgg ageeeetgga eggteeagea ggtgetgtee tggagtgeet1200
 ggtgttgtcc tccggaatgc tggtgccgga actcgctatc cctgttgtct acctgctggg1260
 ggcactgace atgetgagtg aaacgcagca caagetgetg geggaggege tggagtegca1320
 gaccetgttg gggccgctcg agetggtggg cagcetettg gagcagagtg cecegtggca1380
 qqaqcqcaga ccatqtccct gcccccqgg ctcctqgqga acaqctqgqg cgaaqgaqca1440
 ccqqcctqqq tcttqctqqa cqaqtqtqqc ctaqaqctqq qqqaqqacac tccccacqtq1500
 tgctgggage cgcaggeeca gggeegeatg tgtgeactet aegeeteect ggeactgeta1560
 teaggactga gecaggagee ceactageet gtgeeeggge atggeetgge ageteteeag1620
 cagggcagag tgtttgccca ccagctgcta gccctaggaa ggccaggagc ccagtagcca1680
 tgtggccagt ctaccatggg gcccaggagt tggggaaaca caataaaggt ggcatacgaa1740
 gga
```



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 970 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

eggetegagt gggtttttag tttgtteett etttttgaag teeetteatt teaateettg 60 actetetete coetteeett geccagetet gttgaatget getgtgegeg tgtgagggee120 gctctgcaca cagggccctt gggttgtgtg aactgaaatt ctccctgtat ttgtgagact180 cgcaggagtc cccatctgta gcacaggcaa tgccagtgcc atgctgcagc ctcagaaacc240 aggeetetea etecageage aggeagaace gtgtetgtgg tegggtgetg tecacagete300 tgtctgcctt gttcttgggc ttgagctgga tagaggtggg gtctcttcac cttccctgaa360 ttcagaacag accetgtgcc tggccccagt gtgcccaggc aattccccag gccctcattg420 ggagecettg gtgttetgag eageagggee eaggeageae atgageagtg eeeagggget480 ccctqcqtqa ggacqgcaag gtgcgatgta tgtctaactt attgatggca ggcagccccc540 tqtqccccct aagcctggcc ctggttattg ctgagctctg tgctcagtgc tgcggcctgg600 ccqtqqctcq tctqttcctt tggggggccc gggcgggttg tgggaatcag tcttcacaga660 cagacgtgag ccaggcggag gactcgttcc ttgcagaggt cagtcctcac ctgcaggtgt720 eggggtgggg ggggcaagg aggggcaggc acacaccatg tetgacetga accegattet780 ggggagcatc ttcccgctcc ggccccacga cctccacagg gttacattgt aatatatatg840 ccccagctaa cctgtctgat ggtggcatct tcctgcagac atttcaaaca tgtaactttt900 aaaaaaaaa

- (2) INFORMATION ON SEQ ID NO. 15:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2003 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```
gagagatetg aaataacett teecagtggg cagggttgee agggttgagg ggacageaca
taccaccccc acccaacctg ttcgaggggc cctgcatggc acgggatgag tccctgccct 120
gtgcagctgc ctggcagtgg ctgggacaag gatcttgcag ccagcacaga ggcctcttca 180
aaggeetete eetettggea etecaggeaa ggeaggtgee egetteeeca acacetecag 240
gcagtgacce tagggcatge eccageaggt eteegageag ceaetgggae eegteteage 300
acatectgge etttgaaagt etgatateet gagaggaggg eaggttttag ggeegeagtt 360
ccagccageg tecccageet ggetteeetg ccatggaete agtagetegt ggggettett 420
accacccacc agccccgctg gggtgcggcc tggctgtggg caaaggagga cttgcctgga 480
gatttgagag aagatteett etaccaggge tgetgagggg ceaggeetge atcagggget 540
aggetetgge tgggeeegga ggetgagaet aaggettteg accetggtge etecatgtgg 600
atgctgcctc agacaaaggc agtgagcctt ccctgccaaa gtgcccatcc catgggctcg 660
geeteactgg teactgttag eccatgaaca egtgtgggee teggteacgt ggetttgagg 720
gcagtctgac caggctagac cacacgtgcc gtgacagggg gtgccattcc cctcgcaggc 780
tctaatgtgc ccacatgtag cctggcagtc caaagaccaa gaatcaactt gcaaatctgc 840
cattaaactg ctgtgcgact tcaggcatat cactgccttc tctgggcttc agtgtccttt 900
tcatacctag aagtctgcgg tctgaggctc tttgggttca gacacactgt tctaggcttc 960
tgtaggggac cttgtgatct gccgtgcccc tcctccctgt tcttttctgt cctccccacc1020
ccacceteag aagetgettg etetgeeece aggacaggag ettgaeggat gaagtgeage1080
cagccaccca ggtgccattt ccagtctgac ttccagaaat gtgcaccatg tcctagagca1140
cagacccatt ggctggagcc tcctgggagg gttcaaacca tcagctctat gagaaatgcc1200
cagaaagget ttgccgacte catecgtetg tggaggetge ctgcctccgg ggtgggatgg1260
gtggtttctc ctccaattca gacccaagag gtagcccccg agggcatgta cctggtggga1320
agcageteag gtaccettgg gggttgeagg gecettaege aggtatttet etetetee1380
tetetggggt gegtgtgtge gtgegegtgt gegtgeetat gettttetet gtgggeacat1440
caggatgccc ctcggagagc atgtgcacgt gtccccacct gagcgagcgt gtgtgtgtgc1500
tectetgegt eccaggiting gaegictagg gittgging ectgicitet geceteeetg1560
agcccacagg gtcagtcaat gtatcttcta cgtgcctctc cctctgcctt ctctcacagt1620
gccccggct ccagagctca ggggtagggg ttctcctgag ggtgcagggg atccttctca1680
tetectggae cetecaggge actetggtee etattececa getectagge agetgagecg1740
ggtcccttag gggaggtgac caggagcttt ggtgcaggga gctcttggtg gggcaaaggg1800
ctggacccct gccaggtctg tggacatggt tatatgcccg ggagaggggg gtgcagggcc1860
ccagggatgg cccccaatcc cacctctgtt tattctgtaa actgcaacct ataaataacc1920
tttagcattc ctattgtaac aaaattaatt tttatgaaat aaattatatt tcctagtcta1980
                                                                  2003
ataaaaaaaa aaaaaaaaaa aaa
```

(2) INFORMATION ON SEQ ID NO. 16:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2279 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

gattgaatta agcccttggg tttgccccac tgcagcttca agcggaaagg aaggaaccag ttggaccagt ggtcacagac ccaagcaaaa ggcgaccgca atcagcagct gggtctcacc 120 cettteetet gaaccagtga eccaaacett teaccetega ttgggeaace ttggeetggg 180 gcatgtttat caccactgaa gtgacttgca gctatcaaag accagttaga gggtgtgcag 240 caagcacttt ctcaggctgc ccccatccca gaagaggaca cagacactga agaaggtgat 300 gactttgaac tacttgacca gtcagagctg gatcaaattg agagtgaatt gggacttaca 360 caagaccagg aagcagaagc acagcaaaat aagaagtett caggttteet tteaaatetg 420 ctgggaggcc attaatctag gaatcagctt gcaacagagc acaaaaaaca ccaaaaaaat 480 ttcaaacaaa aaaaaaaaa aaaaaaggaa aagaaaaaaa ttgaactgta agctttaatg 540 attactttag atttgtttta ttttccctcc tgcagtgaat taattggata tatatcagct 600 gacactgata gattgatatt totgatogtt atttttgtgt aataagcatg gaaatgaact 660 ttatacacac cactgtgttg tcagagataa atattagggg ttgtttttaa agcaaaaaga 720 aaaaaacaaa aaccaaacta ttaaaatcct cctataaata ttctttttct ttacagtttt 780 tcaagcatgc aaaacagttt attgtaactt actgaaaaat attaacaatt aattgtgaat 840 acatgctgtt accagcttcc ttattcctaa tacctggaaa atttttttt caacggatag 900 attttgatgt aaaaaagacc gaaattatca aggtatctta gttgaaggac ttgggaaata 960 ctatcaaaat taatttctta ggaaaaaatt taaaagtata tttaagtact ctggatagac1020 tgaaacgttt ccatgttatt tctgcagttg tagacttagg cttatttgta aagaagcatg1080 ctccattgac tgccatctct agtcttgcag tgggtggtat taacccatag aaagcaagcall40 gttgtgtatc acatagacaa tggttatgat gtaaacagat tcagttgttt tgttgttcat1200 togtcatatg tttgtgatag ggatgttggg agcacagete tattetgeet getcagaett1260 aagttagacc cttatctttt atattatgtc atgaaaaaag tctcctaaaa ttgtgaaact1320 agttcttgat gagtgatgtg atcatcagca ataaagatat aataactctg ttttcttagc1380 ctgtatagag gagaggaact tgcttggctt taaaatatat ttatttgcca tttaagtata1440 aatatgaaat ctgtttctta ttgggaagat agaatatata tattttcctt taaacttttt1500 aaggtcactt ttaaataacc aaatttgatt tatggttttt aacaaaggac taaagagctg1560 aaaccaacct agttttgttt ttgtgatata aactttaagt gtcgagggac catgccagca1620 actaccaaaa atctcttaaa tcttcaggta cagctggcat tttggcagat gcatagagac1680 atctgagacc ctcagaaagg aaggataatc caagaatata ggaaatctgt gttctcttcc1740 tttcatttta tcccttatat ttctaaagac taattataag taatctgaca ttttaatgta1800 gctactctta tttatttttt ctttctgagg tattaaaata tctggactga gttttgccaa1860 atgttaaagg gagaagagtt actgaagact ttgaacactt gctttttgtg attgcttatg1920 tcattagtgc ctcatgactg tgtttgatgt cctttattga tacaaagtga gcctgtgcct1980 tcattatctt gcccatttta atacaaatgg aaacctggtg tttgaaaatc tctgaactgt2040 gtgggttttg gaggaatata cctgaatttt attcaataac agtttctgga caggaagaaa2100 aatacagtta catatttata aaatagtcgt tatcagtatt tttttatgtg tatgtttctt2160 totttaaaac aatattottg gatataaagt agaaaagttt aaaggtoatt tocatttott2220 cactaaggag aaaaaaagtt aaataatcca agtaattaaa gatataagtc actagatga 2279

- (2) INFORMATION ON SEQ ID NO. 17:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 761 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

aaatcttagg gtaagccagc tgccttggaa gcccaccagg gctccagact gcagggaaga 60 agccgggagc aggcagccat acctccactc ttgtcctcaa ggactcagct gtgtggcctt120 ggatttcttt ttgcgggact tgcgccctgc aggacactgg tgttggagtt ggagggtcct180 atcctgccca ggggtgactc ccagggttgc agggggataag ggtggagaag ggtgctgtag240 cccttgcagg cgtgaagtcc tttctgctct cttagcctat tacattagga gtggctgtag240 cttgggttgc aacggtccag gatccccca aaatgggatg gggataattc aggaatcag360 ctgggttggc acagggggg tattccttgg agaggcagga ctcacacaca cccatccaga420 tcagtgtagc ttctccctta ggaagcctct aggacatccc ccatgttaga gtccacatca480 gcaaagctgc tctgcccttg gctactttca cttgggctac ctgccttggg ctacttccac540 tagctgcaac cctgggacgc atgggaggg aggggtgta ccctcaggaa cagtgtggtc600 cttggagggt ctagcagac cctgagcatc accacccag ttattgtgac cccacgtttc660 cacccatcag ccatgggg tctctgcctg tgtgaacagt agggcccaac ctggaaccag720 atggtacggc catgccggtc ctgcaggag ctcatgcctg g

- (2) INFORMATION ON SEQ ID NO. 18:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1403 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

ggtggctttg cctgggtgct gggcctgcgt tctctggctg cttgctgcct gtgtgcgttc 60 cttggtggct ttggcttctg cactccttgg tcgtcaccgc tcaggtcctc cattcacacg 120 aggteetect egetetggee getettgetg etectgtetg aagaaateag aetgatttee 180 tcttaagact cctagggatg tggtgaagag ctgggactca agtgcagtcc acggtgtgaa 240 acatgaggga ggtgaggtgt ccgtccactt cccccataaa ggtgtgcatt tcagttaggc 300 tgccccgcca cagagcaggc ttcatctgct ctgccatcca gccccatctg gatgtgaggt 360 ggggtggaga catcatgggg tgattgcaga aagggggagt ggcggcccac gcagcttctg 420 ctgaggaget gaccgetetg agetgttetg tttegtattg etgetetgtg tetgeatgta 480 ttgtgaccgt gcggctccac ctcttccagc tgctgctaca gctgaggcct ggatcccggc 540 ctttccctgt gacttacgtg tctgtcaccg gcaggcagcc ctacaaatcc tggtgacctg 600 ctctcccaag aacagagcct gtccccagat gtcccagtag cgatgagtaa cagaggtggc 660 tgtggacttc ctctacttct ccttgctgga tcagggcctt cctgcctccc gctgggcagg 720 totggeettg etetettgge agggeecag eccetetgae eactetgeag eteaceatge 780 agetgatgee aaagttgtgg tgtecagtgt geageageee tgggageeae tgecaeette 840 agaggggttc cttgctgaga cccacattgc ttcacctggc cccaccatgg ctgcttgcct 900 ggcccaacct agcgttctgt gccatgctag agcttgagct gttgctcttc ttcaggggag 960 gaaatagggt ggagagcggg aagggtcttg ctcctaagtg ttgctgctgt ggcttttttg1020 cettetecaa aqacqcaetq ecaqqtecca agetteaqae tqetqtqett aqtaaqcaaq1080 tgagaageet ggggtttgga geecaectae tetetggeag cateageate etaeteetgg1140 caacatcagg ccaacgtcca ccccagcctc acattgccag atgttggcag aagggctaat1200 attgaccgtc ttgactggct ggagccttca aagccactgg gatgtcctcc aggcacctgg1260 qtcccatgac cagctccccg tctccatagg ggtaggcatt tcactggttt atgaagctcg1320 aqtttcatta aatatgttaa gaatcaaaac tgtctttgtt caggctgcta taacaaaaat1380 ataatagcct gggtggctta aac

- (2) INFORMATION ON SEQ ID NO. 19:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1702 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```
qqqccqcacc qqaqtqtcqq tqqtqatqqq catcccqaqc qtqcqqcqcq aqqtqcactc > 60
gtacctgact gacactctgc actcgctcat ctccgagctg agcccgcagg agaaggagga 120
cteggtcate gtggtgctga tegeogagae tgaetcaeag taeaettegg eagtgaeaga 180
gaacatcaag goottgttoc coacggagat coattotggg ctcctggagg toatotcacc 240
ctcccccac ttctaccctg acttctcccg cctccgagag tcctttgggg accccaagga 300
gagagtcagg tggaggacca aacagaacct cgattactgc ttcctcatga tgtacgcgca 360
gtccaaaggc atctactacg tgcagctgga ggatgacatc gtggccaagc ccaactacct 420
gagcaccatg aagaactttg cactgcagca gccttcagag gactggatga tcctggagtt 480
ctcccagctg ggcttcattg gtaagatgtt caagtcgctg gacctgagcc tgattgtaga 540
gttcattctc atgttctacc gggacaagcc catcgactgg ctcctggacc atattctgtg 600
qqtqaaaqtc tgcaacccg agaaggatgc gaagactgtg accggcagaa agccaacctg 660
cggatccgct tcaaaccgtc cctcttccag cacgtgggca ctcactcctc gctggctggc 720
aagatccaga aactgaagga caaagacttt ggaaagcagg cgctgcggaa ggagcatgtg 780
aacccgccag cagaggtgag cacgagcctg aagacatacc agcacttcac cctggagaaa 840
gectacetge gegaggaett ettetgggee tteaceetg eegeggggga etteateege 900
ttccgcttct tccaacctct aagactggag cggttcttct tccgcagtgg gaacatcgag 960
caccoggagg acaagetett caacacgtet gtggaggtge tgccettega caacceteag1020
tcagacaagg aggccctgca ggagggccgc accgccaccc tccggtaccc tcggagcccc1080
gacggctacc tccagatcgg ctccttctac aagggagtgg cagagggaga ggtggacccal140
geetteggee etetggaage actgegeete tegateeaga eggaeteese tgtgtgggtg1200
attotgagog agatottoot gaaaaaggoo gactaagotg ogggottotg agggtaccot1260
gtggccagcc ctgaagccca catttctggg ggtgtcgtca ctgccgtccc cggagggcca1320
gatacggccc cgcccaaagg gttctgcctg gcgtcgggct tgggccggcc tggggtccgc1380
cgctggcccg gaggccctag gagctggtgc tgccccgcc cgccgggccg cggaggaggc1440
aggcggcccc cacactgtgc ctgaggcccg gaaccgttcg caccccgcct gccccagtca1500
ggccgtttta gaagagcttt tacttgggcg cccgccgtct ctggcgcgaa cactggaatg1560
catatactac tttatgtgct gtgtttttta ttcttggata catttgattt tttcacgtaal620
qtccacatat acttctataa gagcgtgact tgtaataaag ggttaatgaa gaaaaaaaaa1680
                                                                  1702
aaaaaaaaa aaaaaaaaaa aa
```

- (2) INFORMATION ON SEQ ID NO. 20:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 802 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

- (2) INFORMATION ON SEQ ID NO. 21:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1647 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```
acceptate thickthic cointition thickthit gggtaaggit gacacecat
ttattqqaqa agaccccaqc acccgccccc tgaggtctta agggctttgg tgtatccttg 120
gtcacgagcg ctgggccagg aagcagagtt cctgagagcc aagtctagtg gttgagagag 180
gaccetgget gggeetgggg ageaggaage catetgteea getgggeage eeccatgggt 240
ccctggtgca gccccggcca tgtgtccagc gccccatact ccatgagggg ggtctgcacc 300
ccatcacacg ctggttctgc aggtctgcac ccctgtgagg ctgcccctgg ggggcatggg 360
ttctgttggg ctcttgctcc cagcatggat gacccagcga tagcagtcag tgatgcgctt 420
gttgggtgca tgggggccac agcgggtgca gtacacgatg cccagtgcaa gcaggaccac 480
caaaaagaca cacgttggca ccaggagtgc caccagcagc caccggtcat ccctctggct 540
gtgctcggca agaccagcct cccccagggc tgttgggggct gctgtgggag ctggtgaggg 600
cagecacagg gecaacttgg gactggggee atetteeett gggatttggg gggetttgga 660
atggggatgt gtagggctga tgggtgaggt ctggttagtg gggctctgag agggcaggag 720
ggtggggagg gctgcgggct gggtggcagc aggcacagag atttgatggg caggagacac 780
aggggacctg gaggtggtgg tcagagaggg ctgggcagtt gggataatgg gaagctgggt 840
ggcctgggtt ctgaggacaa gggcatctgg ggcttgaggg ggtcgctggg caccgagggt 900
ggtgaccaga ggggcatggt taggtgggat tccaggcaaa tgagtggtgg tctgggtgcc 960
agcgacccgg gtgtctggaa acatggggga ctggtgggca gggaagagct ccggatattt1020
ggttgagatc atagggggct ggtgggcagg aggctgtgct gaatgagaga cagagagaat1080
accgggttgg taggcagaag gcagatctgg atagttggct gcgatcacgg ggatctggtg1140
qtcacqqqac aaaqctqqqt gtqtqqcaqq gatcacaqqa qqctqqtqqq caqaaqqcaq1200
tqtqqqatqc qtqqcaqaqa ccaccacaqq ccqqqtqacq qaqaqcactq aqqaqtqqta1260
ggggaccctg ggggcactga gcgggggtgg ccaggtgggc tccgggtagg gtatctgtgg1320
ctctctgtcc tctgggaagc tcggtctata ggccagggca aagtcaggcg gctgcgtagg1380
ctccatccac aggateccag geateteegt ecagecaceg ttgaageett ccaggeeteg1440
tetteatett ceteateete ceegteatee ageaacteat eteegaggte etgggaacee1500
tgggcaccca tggcccctgc agggctgcag ctgatgccat cagcctccag ctcatgtccc1560
tegetacaat aacactegaa gecaceaacg tagttgacae acatetgetg geacacaceg1620
                                                                 1647
gcaatctggc actcatctgt gtccaca
```

- (2) INFORMATION ON SEQ ID NO: 22:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1170 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO.
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```
cctcgctggc agaagagata gaatcagggc tgcccccaca gagtgggacc caaggggcta
attggaggca cgaggggacc cctccccagg gccttttcct cctctgcgtc ttccatctac 120
tgaaatggga gaggggtgg ggagcttctg ttctggtgaa gggacccggg caggccccca 180
gcaccccatg ctgacttgga gaaccccaga tctctggggc ccagccaggc agggtgtggg 240
ggcagetgtg ccaatetace teacaggeee acceetgee gggcatgeeg tgggateatg 300
qqcaqqqaaq gctctgqggg tcggagacac cgctgcttag cacccccagc cagaacaccc 360
tqaqqqtctc qgggctctgg agagagtggg qcgggaggaa gaattggcac cttcctaggg 420
aaqqaqacqa qcqcttcqcc ttgattctcc gagaaqcctc cgagaagtgc tttaagtgtg 480
tttgcatgcg ccaggcggtg ggcagcgggg gcctgtccag ccctctcccg ccatccttcc 540
ccaagtgacg tocactgcct tgtcaccage gacetgcctg tcatgcccac cccctgagga 600
agcatgggga ccctaacacc ctggtgccct gcaccagaca ggccgtggtc aggcccaggc 660
caccqqccqq gttctqccac agcttcccac gtgcttqctq acatqcqtqt gcctqtqtt 720
ggtgtctgtt gctgtgtcgt gaaactgtga ccatcactca gtccaaacaa gtgagtggcc 780
ctcgaggcca cagttatgca actttcagtg tgtgtcataa cgacgtcact gctttttaaa 840
ctcgataact ctttatttta gtaaaatgcc caggagtcct ggaagctacg cggacttgca 900
gaggttttat tttttggcct tagaatctgc agaaattagg aggcaccgag cccagcgcag 960
cagcctcgga cccggattgc gtttgcctta gcggatatgt ttatacagat gaatataaaa1020
tgtttttttc tttgggcttt ttgcttcttt tttccccccc ttctcacctt cccttctccc1080
cgaccccacc ccccaaaaaa gctacttctt cattccgtgg tacgattatt ttttttaact1140
aaaggaagat aaaattctat attcttaaaa
                                                                 1170
```

- (2) INFORMATION ON SEQ ID NO. 23:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1259 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```
ggagtatcca gataggcgac acgccggcgg gcggctgagg cgggaatggc tgctgtactg
cagegegteg ageggetgte caategagte gtgegtgtgt tgggetgtaa eeegggteee 120
atgaccetce aaggeaccaa cacetaceta gtggggaceg geeccaggag aateeteatt 180
gacactggag aaccagcaat tocagaatac atcagctgtt taaagcaggc totaactgaa 240
tttaacacag caatccagga aattgtagtg actcactggc accgagatca ttctggaggc 300
ataggagata tttgtaaaag catcaataat gacactacct attgcattaa aaaactccca 360
cggaatcctc agagagaaga aattatagga aatggagagc aacaatatgt ttatctgaaa 420
gatggagatg tgattaagac tgagggagcc actctaagag ttctatatac ccctggccac 480
actgatgatc acatggctct actcttagaa gaggaaaatg ctatcttttc tggagattgc 540
atcctagggg aaggaacaac ggtatttgaa gacctctatg attatatgaa ctctttaaaa 600
gagttattga aaatcaaagc tgatattata tatccaggac atggcccagt aattcataat 660
getgaageta aaatteaaca atacatttet cacagaaata ttegagagea geaaattett 720
acattatttc gtgagaactt tgagaaatca tttacagtaa tggagcttgt aaaaattatt 780
tacaagaata ctcctgagaa tttacatgaa atggctaaac ataatctctt acttcatttg 840
aaaaaactag aaaaagaagg aaaaatattt agcaacacag atcctgacaa gaaatggaaa 900
gctcatcttt agtttcagat taaagaaagc tttgttttat tttgctttga gagaatggta 960
tgttttctta actataggtt attttataga gaatataaaa gtataaaaca ttaaaaataa1020
coctagatat actttaaaat aatgttatat ttatgctaaa atatgtaaat tacactatac1080
aaccatatga taggttattt ctctaacctt gtcttctaac gttttaccaa aaattcataal140
tctaatagtt tatcagtttt caatagatta aataaaatga ttactttaaa aataataaaa1200
tttatctaat ttaaagttga aaaaattttt ggccgttagt tatctattac tagtgatca 1259
```

- (2) INFORMATION ON SEQ ID NO. 24:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1021 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
gegtteetee teeggeeete ggteaeegee ageaegegee tgetteeegt etgegegagt
ccacgcaget ecccaggee tteaccagea cagcageage aggeatggea geaagegtgg 120
agcagegega gggcaccate caggtgeagg gecaggeeet ettetteega gaggeeetge 180
ccggcagtgg gcaggctcgc ttctctgtac tgctgctgca tggtattcgc ttctcctccg 240
agacetggca gaacetgggt acactgcaca ggctggccca ggctggctac cgggctgtgg 300
ccattgacct gccaggtctg gggcactcca aggaagcagc agcccctgcc cctattgggg 360
agetggeece tggeagette etggeggetg tggtggatge ettggagetg ggeeceeegg 420
ttgtgatcag tccatcactg agtggcatgt actccctgcc cttcctcacg gcccctggct 480
cccagetece gggetttgtg ccagtggeee ecatetgeae tgacaaaate aatgetgeea 540
actatgccag tgtgaagact ccagctctga ttgtatatgg agaccaggac cccatgggtc 600
agaccagett tgageacetg aagcagetge ceaaccaceg ggtgetgate atgaaggggg 660
eggggcacce etgttacetg gacaaaccag aggagtggca tacagggetg etggacttee 720
tgcaggggct ccagtgaagc ccagcactgc tgcagggggt gggctgcctg cctgctctga 780
getetetett geaegetete tettetete caggetetgg eteatgeaca tgeaacaggt 840
gegtetgtet atatgtetgg gttettgtet tttgtggtet gtttgtettt tetacetett 900
tetettgeag tgatagactg agggggtaaa atcaagagga aaaaactete aggaateaag 960
gaacataatc ctgtggaggg taaaccatta catgaggctt ctcccgggtc gttcaagttt1020
```

(2) INFORMATION ON SEQ ID NO. 25:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1407 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```
agcaaaggtt geeggagaee aagateggaa gegtgaaata egaaggeate gagtteattt
aactgaaaac cggctcaagg agcaaggcca tcaggactca gcttttataa aaacaagagg 120
agtgcacttt tgttttgttt tgttcttttt ggaactgtgc ctgggttgga ggtctggaca 180
gggageccag tecegggece catagtggtg egggeactgg acceeeggge eccaeggagg 240
ecgeggtetg aactgettte catgetgeea tetggtggtg attteggtea etteaggeat 300
tgactcaagg cetgectaac tggctgggte gtttetteea teegaceteg tttetttet 360
ttcctatgtt cttttgttca gtgaatatcc ctagagctcc taccatatgt caggccctat 420
gecteacet gagaacgeag tgggeatgag gtggaeetgt ttgetgggaa ceceaggtea 480
eccepttte ttectactet gtgeetggag cateatgtee acceptgeag atecttggaa 540
aagaaaatgt ttatgttgca gggtattgca tggtcacgag tgagggcagg cccctgggga 600
cacatotgee cacagetgea caggecaggg egeaggeaca tetgttggtt eteaggeete 660
agataaaacc atctccgcat catatggcca gtgaccgctt tctcccttca agaaaattct 720
gtggctgtgc agtactttga agttttaatt attaacctgc tttaattaaa gcagtttcct 780
ttcttataaa gtggaatcac caaatcttat cacacagage acagtcctgt agttacccag 840
cecgetecag cagtgeggga gattgtaagg aageggtgge ggetggtgaa gcaagtetea 900
catgtcggcg ttcttggcca atggatacaa agataaagaa aatgttgcct ttttctagga 960
actgtcagaa atcctcatgc ctttcaagac ttctgtgaat gacttgaatt ttttattccc1020
tgcctagggt ctgtgaacga ggcctgtctc ttccctgggg tttctttcca tggcctttat1080
ttctcctctt ccagtgggag ttttgcaggc tcttctctgt ggaaacttca cgagcgttgg1140
ctgggcctcg gcttcgctgg agtgtactcc agggtgaagg cagagtggga tttgagaccc1200
aggitaggca cgacccaggc tgagaaggga cgtttccatc attcacagtg ccctcccac1260
agcactacet cagecegage eccacectea etectacece acceegegat egteaggggt1320
gccacggtgg gccggagggt gccccgtcgg ggcttgttcc tgttgccggt ccctgaaaaa1380
                                                                  1407
gcttttcccc ttttgaaatt caagcac
```

- (2) INFORMATION ON SEQ ID NO. 26:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ctctcggetc cgcctggcag cagetccgcc gcccagaggc gtccgagacc ctccgactcg 60 tgggtacgca taggcctcgc cagegagcct tgcccaggca acgagtcgcc agcccgccc120 ctcgccgcgg gctaggtctc acctcgccac cagtacgtct tggacaagta gtgccaggtc180 tgatgccggg tgtggtgagt gccgccggga cccaggtgcg ccgcctcgat gaggtcccgg240 cgtcgctccg gctgcagcac cacetccage tccgcgaagg tcttgc 286

- (2) INFORMATION ON SEQ ID NO. 27:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 815 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

(2) INFORMATION ON SEQ ID NO. 28:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 548 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

tttctcgaac cttctcttt ctttctttt tgcactgtgc aaatatattg actttatttg 60 tctcctttca ggagcctcac agacatatcc aggtaaaaag atcgttaaat aaatgccttc120 agccatcgca atgcaaaaat aaatatcaat cctccagacg cagtagcagc cgcgctgcgc180 ccaaagtccc aacggccacg cctaacaatt ataaaagtgt tcagcgagag tgttggcgt240 agtgtgaatg agtgtgcac ggggggcacg gtggagcggt gtgcaaaatc ggagttgcaa300 accatcggac aagggcatgg agtggctacc cgccgccgac tcagcggggg cgcgcctccc360 cgcacacact cacagcagag ttcgcactgg gaagagttaa aaaataaaca tttacaagga420 cgagcgagt cgcaccggt cgcgcctcc cgggccagg cgagcgcgc gaggggcgca480 ccgaccggt cgcagcggc cgggagtccg aagcgcgca ggagcgcca ggagcgcagg cggggggcs480 cttgcggg

- (2) INFORMATION ON SEQ ID NO. 29:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

geaagatgge tgeectgaca geggagattt tgeageacte cagageetge teaaggeete 60 ctegaaagat gttgteagae agetgtgtea agaaagettt teeagtteag eeettggett120 gaaaaaacte ttggatgtta catgtteeag ettgtetgtg acceaggagg aggeagagga180 actgeteeag geeteactag getggtggea tteegtgace tgteetee240 cgaggeaatt etggetetet tteeagaaaa ttteeaceaa aaceteaaaa acetgetgac300 aaagateate etggetegate tggaetggag aggaacegaa geecaggeaa ateagatete360 tetgeeacge etggtegate tggaetggag agtggatate aaaaceteet cagaeageat420 cageegeatg geegttgee eacetggeet ggtteeagat ggaaggtte480 ceaggetatg ggg

- (2) INFORMATION ON SEQ ID NO. 30:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1063 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN

- (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```
cgcctccccc tccaactctc aacccacttc tccagccagc gccccagccc tcccgccgcc
cgctcgcagg tcccgaggag cgcagactgt gtccctgaca atgggaacag ccgacagtga 120
tgagatggcc ccggaggccc cacagcacac ccacatcgat gtgcacatcc accaggagtc 180
tgccctggcc aagctcctgc tcacctgctg ctctgcgctg cggccccggg ccacccaggc 240
caqqqqcaqc aqccggctgc tggtggcctc gtgggtgatg cagatcgtgc tggggatctt 300
qaqtqcaqtc ctaggaggat ttttctacat ccgcgactac accetecteg tcaceteggg 360
agetgecate tggacagggg etgtggetgt getggetgga getgetgeet teatttacga 420
gaaacggggt ggtacatact gggccctgct gaggactctg ctagcgctgg cagctttctc 480
cacagocato gotgocotoa aactitggaa tgaagatito ogatatggot actottatta 540
caacagtgcc tgccgcatct ccagctcgag tgactggaac actccagccc ccactcagag 600
tccagaagaa gtcagaaggc tacacctatg tacctccttc atggacatgc tgaaggcctt 660
gttcagaacc cttcaggcca tgctcttggg tgtctggatt ctgctgcttc tggcatctct 720
ggcccctctg tggctgtact gctggagaat gttcccaacc aaagggaaaa gagaccagaa 780
ggaaatgttg gaagtgagtg gaatctagcc atgcctctcc tgattattag tgcctggtgc 840
ttctgcaccg ggcgtccctg catctgactg ctggaagaag aaccagactg aggaaaagag 900
getetteaac agececagtt atectggeec catgacegtg gecacageec tgetecagea 960
geacttgeec attecttaca eccetteece atectgetee getteatgte eccteetgag1020
tagtcatgtg ataataaact ctcatgttat tgttcccaaa aaa
```

- (2) INFORMATION ON SEQ ID NO. 31:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 472 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```
cggctcgagg cggcgatg gcggcgggc tggcgcggct cctgttgctc ctcgggctct 60 cggccggcgg gcccgcgcc gcaggtgcag cgaagatgaa ggtggtggag gagcccaacg120 cgtttggggt gaacaacccg ttcttgcctc aggccagtcg cctccaggcc aagagggatc180 cttcacccgt gtctggaccc gtgcatctct tccgactctc gggcaagtgc ttcagcctgg240 tggagtccac gtacaagtat gagttctgcc cgttccacaa cgtgacccag cacgagcaga300 ccttccgctg gaacgcctac agtgggatcc tcggcatctg gcacgagtgg gagatcgcca360 acaacacctt cacgggcatg tggagagc cgagcaactg cgtctaaggg gt 472
```

(2) INFORMATION ON SEQ ID NO. 32:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2568 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
catctetetg cagtgeeete etegeetgtg cagecegege acceaeagge teacceetee 60
tgcgggctgc cagaagcccc ctccagcagg gcctctctcc gtggccccag cttcactctc 120
teceteagea catgecetge tggaggeece ageceteegt ggacageagg ggeeaegtgg 180
agecegggee geteaceege gacceagtge tggeegeett ettggtgeea aaceeeette 240
ccccacccag agactgggca gctgtgtctg gttcgttctt tgcactaacc acatttgtca 300
tetetaggge aggetgggge tgegggetga gggggaeege tggeaeeeee etteeeteee 360
ttottggtto catttocato catgacaggt acagcatoco aggagecegg cetgagggge 420
tggacccgag ccggctgtga acatccctca gcccctgctg tccccccttg ggactaacca 480
ctaacctcac ccccaaactc cacgggtgcc cctagctggc ccagagccgg cagtgtgagc 540
ccaagtccgg gctggagccg aggccggagc agctgtctgg gagtcaaggc tgcagtagcg 600
tttcttcatg gggtgctcca gggggtgcca cagaccgaca ggcagcccaa gggcctggac 660
accectecce aggeaggtge tgeeccagga ggaetgteet egggaatgaa eeteeegegg 720
getttggact gaggteectg tggeeteggt etecteecea tgaagtggga gegaggetee 780
ccaatggtgc ttttggcttt agtgtacgat gtttgctgtg cttcccgccg tggagggcag 840
agecacecca cateaggate ggaegtgeta ececteeegg teeeggeeet ggeeeageea 900
gcccagccct cgaggctcga tgcctgtgcc aaggccaggg gcagccagag ggcagctgga 960
tggccacgtg caggggtcaa ggctgggccc tgcagtgggg cgggccgcca gccccagcag1020
tttacagacg catggctctt cctcccagag cagccggcag ctacctggac cggaaatgtc1080
ctcatcccct ccctggggcc aggetetgcc ctggccttcc tctgtgaacc cctcctttct1140
ttgtgctggt gtctgggacc aaaaaggggg aatatgggag ggcagagtgg ggaggggagt1200
ccatgggcct ggggccccaa gccggggcgt ctgagctccc caggcatgac caaacctcag1260
tggagggcc tctgcttcag gccccgcctg gctgacattc tgagcccccc tcggaggccc1320
cgccacagec aacetgeeca gtettteete tgggettgae eegeeaggga gtteteeagg1380
cctagggcca ggagagaggc cctggcaccc tggcgtgggt gcccgccaaa cgccctgcga1440
ccgctcagaa gcacaaatgc tgtccatggc cgtgaggctg cctgccaggt gaatggacat1500
agcgtgagag gcggtgaggc cagggcttcc agcctcgtgc tgtctcggga ctcctgaccg1560
tggtgtgcgt gtgtgcccgt ctgtgacttt ctactcacca aggttgaaga aaggaaacgg1620
ggaaaatcaa aaggggttca aaccccacct cagtaggtgg aggggagcgc ctgccattgg1680
ttgtattttt gttctgagtt ttcggtgccg tgttcctaac tactccatcc catgacctcg1740
ccacacctac tggggcatct ggctggtgcc tgctgccatg gccagccccc actctcaccc1800
tgcacagggg gtcttgcagc ccccaggccc acagcctcgt tgggaggaca gggtggccct1860
ggggacaaga gggaggagcc caggggctta cctcactgag agtgctcccc agcaggcatc1920
cactacccca gggcccccca catgtcatgg caaggttggt agtgaatggg cctggttggg1980
agcageceet ggeceattge ecacecacee ateteaetat geaattegag ttecaagcaa2040
```

catttgctcc tgccctgggg ccagctctgc cccagccctg agaggggtgg tgaggcagcc2100 ccctggaccc cagaaccca gacaaggggg caggcggggg accagggcct ctcctgtggg2160 atcttgtt tgtgtttaac cataatggtt gtgtactgaa ccacttcata tttgttatat2220 ataatatata tatatataat ctccttaaga ctcagcctcc tggtttaccc ccccggcctg2280 ggcatctgac ctccccacc ccagtgtgat ttaacatcca ggaactgagg cctgaaccat2340 tttgcatttc cccctcctc agcctctgta gggccatggc tgtatgtact gtcgctgtgt2400 tttttgttt ttttagaact gggtttgggg gctgattttt atttctttgg gggcttttt2460 tcttggcaaa tactaaaaat ctcgtcaatg taatttctgt ggtttctatt cagcttgggt2520 ttcatgtttt aaaataaatt ttaaaaagca aaaaaaaaa aaaaaaaa 2568

- (2) INFORMATION ON SEQ ID NO. 33:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

cgcgatggcg gcggggctgg cgcggctcct gttgctcctc gggctctcgg ccggcgggcc 60 cgcgccggca ggtgcagcga agatgaaggt ggtggaggag cccaacgcgt ttgggtgagc120 agcctcgcgg gctggcggct cgagcggggg acggcccggg cccgttcccc gctgaccttg180 ccgcttcccg taggtggaac aacccgttct tgcctcaggc cagtcgcctc caggccaag 239

- (2) INFORMATION ON SEQ ID NO. 34:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

- (2) INFORMATION ON SEQ ID NO. 35:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 641 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

gagagcagta ggtgttagca gcttggtcgc gacaggggcg ctaggtagag cgccgggacc 60 tgtgacaggg ctggtagcag cgcagaggaa aggcggcttt tagccaggta tttcagtgtc120 tgtagacaag atggaatcat ctccatttaa tagacggcaa tggacctcac tatcattgag180 ggtaacagcc aaagaacttt ctcttgtcaa caagaacaag tcatcggcta ttgtggaaat240 attctccaag taccagaaag cagctgaaga aacaaacatg gagaagaaga gaagtaacac300 cgaaaatctc tcccagcact ttagaaaggg gaccctgact gtgttaaaga agaagtggga360 gaacccaggg ctgggagcag agtctcacac agactctcta cggaacagca gcactgagat420 taggcacaga gcagaccatc ctcctgctga agtgacaagc cacgctgctt ctggagccaa480 agctgaccaa gaagaacaaa tccacccag atctagactc aggtcacctc ctgaagccct540 cgttcagggt cgatatcccc acatcaagga cggtgaggat cttaaagacc actcaacaga600 aagtaaaaaa atggaaaatt gtctaggaga atccaggcat g

- (2) INFORMATION ON SEQ ID NO. 36:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

aagttgatga cctacgctct tacttctgct tgccaggagt aactgaaagc aaacaccaca 60 gtctgttgtt tattagcttt taaaggcttg tcaacattcc ttgttaacaa tttctttttg120 ggtagccttt tataaaatgc gtaggtgatg agtgatccag cagacaaggc ggctcgagcc180 gattcggctc gagcggctcg aggtaaaaga aaaaaaatg tggaggaaaa catggcctac240 tcagctttga tggaagtggc tggttactgc ttaatagaga gaatgctttg gaatcctatg300 ttgaaaataa aaagtgtttg gttgtgcagt tatgcggtca tggtcattcc cagacagttg360 gctaaggttt agtggtcctc t

- (2) INFORMATION ON SEQ ID NO. 37:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1539 base pairs
 - (B) TYPE: Nucleic acid

- (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```
ctggggacag gaagcccctg taccattatg gtcggggcat gaatcccgct gacaaaccag 60
cctgggcccg agaggtaaaa gagagaacaa ggatgaacaa gcagcagaac tctcccttgg 120
ccaagagcaa gccaggcagc acggggcctg agcccccaag cccccaggcc tccccagggc 180
coccaggeet eccetgggee eccaaaceet accacaaatt catggeette aagteettig 240
ccgacctccc ccaccgccct ctgctggtcg acctgacagt agaggagggg cagcggctca 300
aggteateta tggetecagt getggettee atgetgtgga tgtegaeteg gggaacaget 360
atgacatota catocotqtg cacatocaga gocagatoac gococatgoc atcatottoc 420
tececaacae egacggeatg gagatgetge tgtgetaega ggaegagggt gtetaegtea 480
acacqtacqq qcqcatcatt aaggatgtgg tqctqcagtq gggggagatq cctacttctg 540
tggcctacat ctgctccaac cagataatgg gctggggtga gaaagccatt gagatccgct 600
ctgtggagac gggccacctc gacggggtct tcatgcacaa acgagctcag aggctcaagt 660
tectgtgtga geggaatgac aaggtgtttt ttgeetcagt eegetetggg ggeageagee 720
aagtttactt catgactctg aaccqtaact gcatcatgaa ctggtgacgg ggccctgggc 780
tagagetate ceacactaga eccagetete eccetaçage caggettece aggecacee 840
tettteeect eeetgggett ttgettttae tggtttgatt teaetggage etgetgggaa 900
cgtgacctct gacccctgat gctttcgtga tcacgtgacc atcctcttcc ccaacatgtc 960
ctcttcccaa aactgtgcct gtccccagct tctggggagg gacacagctt ccccttccca1020
ggaattgagt gggcctagcc cctccccct tttctccatt tgagaggaga gtgcttgggg1080
cttgaacccc ttaccccact gctgctgact gggcagggcc ctggacccct ttatttgcac1140
gtcaggggag ccggctcccc ccttgaatgt accagaccct ggggggggtc actgggccct1200
agatttttgg ggggtcacca gccactccag gggcagggac catttcttca ttttctgaaa1260
gcactttaat gattcccctg ccccaaact ccagggaatg gagggggag cccgccagcc1320
aaaacatgcc ccccattccg gaccccctc tcctcttcta gcccatgccc ttccccggtg1380
gagggaggga gcagggagcc ctcactctcc acgccccttg cttgcatccg catatagtgt1440
gagcagcaag taaccettet ceteetteee cagteaceee teetcaatgt agtggeettg1500
aattgtcttt attaacaaac aggatatcca aggtcgagc
                                                                 1539
```

(2) INFORMATION ON SEQ ID NO. 38:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2195 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 - ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
gctccgagga aggcctgtgg gagtctcgga gacgtgtctg tctgtgaggc gctgggtgca
cgtccccagg gctctgggct aggaaggcag cggcgaggtg cctccccacg tacccctcgc 120
gggcccagcc gagcaacgtg gggcgaaggc ggcggcgaag gcccgggctg ggagcgttgg 180
eggeeggagt eccagecatg geggagtetg tggagegeet geageagegg gteeaggage 240
tggagcggga acttgcccag gagaggagtc tgcaggtccc gaggagcggc gacggagggg 300
gcggccgggt ccgcatcgag aagatgagct cagaggtggt ggattcgaat ccctacagcc 360
gcttgatggc attgaaacga atgggaattg taagcgacta tgagaaaatc cgtacctttg 420
ccgtagcaat agtaggtgtt ggtggagtag gtagtgtgac tgctgaaatg ctgacaagat 480
gtggcattgg taagttgcta ctctttgatt atgacaaggt ggaactagcc aatatgaata 540
gacttttctt ccaacctcat caagcaggat taagtaaagt tcaagcagca gaacatactc 600
tgaggaacat taatcctgat gttctttttg aagtacacaa ctataatata accacagtgg 660
aaaactttca acatttcatg gatagaataa gtaatggtgg gttagaagaa ggaaaacctg 720
ttgatctagt tcttagctgt gtggacaatt ttgaagctcg aatgacaata aatacagctt 780
qtaatgaact tggacaaaca tggatggaat ctggggtcag tgaaaatgca gtttcagggc 840
atatacaget tataatteet ggagaatetg ettgttttge gtgtgeteea ceaettgtag 900
ttgctgcaaa tattgatgaa aagactctga aacgagaagg tgtttgtgca gccagtcttc 960
ctaccactat gggtgtggtt gctgggatct tagtacaaaa cgtgttaaag tttctgttaa1020
attttggtac tgttagtttt taccttggat acaatgcaat gcaggatttt tttcctacta1080
tgtccatgaa gccaaatcct cagtgtgatg acagaaattg caggaagcag caggaggaat1140
ataagaaaaa ggtagcagca ctgcctaaac aagaggttat acaagaagag gaagagataa1200
tccatgaaga taatgaatgg ggtattgagc tggtatctga ggtttcagaa gaggaactga1260
aaaatttttc aggtccagtt ccagacttac ctgaaggaat tacagtggca tacacaattc1320
caaaaaagca agaagattet gteactgagt taacagtgga agattetggt gaaagettgg1380
aagacctcat ggccaaaatg aagaatatgt agataatgga ctgggatata ttgtatttct1440
catgttaaag cctcttccct tgaaattaaa aaaaaatttt aactgataaa acttagggca1500
acattaatta atgtatatto ttacctgaat tgttatactt tttgaaaatc ctgtgacttg1560
cctgtttctc cccgctccaa cgaaatcatt aactctccta aaatgtgttt cattctagta1620-
agaaaacctc aaaggatatt gtaggatata aatcttactt gaaaacatag ctgttgaaat1680
gttttggcct tttggagtgg gggaaggaca aatctgatcc tgtaatcttt ttctttccag1740
taatcccttg tgtctgttgc atgaggacat ggacaataaa gtagtatatg atcctcagat1800
acagggagaa ggacaaggca tacagcttat tgattagagc tggcaagcat ctgctcatta1860
tgtttggaat tgctttctat aagaaaattg cccactacta ctaacttgat caacaatgaa1920
ttcaaaatag ttaacctatg aaataacatc ctctcaaatg tttgctgatg aagtacaagt1980
tgaaatgtag ttattggaaa agtctgtaac ctgtggatca tatatattca aagtgagaca2040
aaggcaaata aaaagcagct attttcatga atagaaaaaa aaaaaatttc aggaagtata2100
aattatatto tgcaccgaac aaggaacaga aattattgca totgtggaag catatatotg2160
ggagttacta ttactttact ggaagggcca agggc
```

- (2) INFORMATION ON SEQ ID NO. 39:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1409 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```
qtttqctqtc cttttttaaa ggattccaaq ccatqtqaaa ttcccttctq qatqtqattc 60
tgggtcgcaa gtccttattt atatgtgagg ctggggaatg ggctgggggt attggcagtc 120
cttttgcagg gcagtgtgtg tggtggggtg acaccgctgt ggcttagccc aaqacactcc 180
cagaggaaaa cactgcagaa ggaactggtt tgcagactgt ggaaggatct gcagttttgt 240
ttttgaccaa aaaaataata ataagttagc tctgaagggc agagggaata cccaagcccc 300
tgatgcctat gagaagtccc tggacttcaa ccctcctgtt gtttggcctt agcccagagg 360
gagctgctca cctgagcacc cttgggggtg ggcagagagg cagggtggga ttttagagtt 420
agtgtctgtg cgggggcagc cctgagcctg gagttgagac tttggggtct cttagtttgg 480
aggtgttgag tgcatttgtg cccctgcctg gttgagagct tcttggtacc tcttgccacc 540
cetteteact geoetgacee aacceeactg gacettgatg etgegaggag tggtgteetg 600
acggaeteag cacteeegee tgatgtattg gateatagga gageaettge teteetgeet 660
ctgccaggag agggcttgtt cctccaactc taggaggcca ggcaagcatg gacaggagcc 720
aagggagcag ggtcattaac tttttcttct ttgcaaagtg ggcacttggc atcagggtcc 780
caatcaccag aaagcaccaa agcccctggc accccaccca ctccatccta cccagggacc 840
ccaagtaggc aactgttatg gcagtgggtc cagcccaggc cagcactgcc agcctcctct 900
ccetgeagta ggeaceaget etaceteece eggeaggeaa tgteetgget teteageeca 960
gcaccatctg ttcccctaga cttctcaggg gccagcccag tctgggccac cctttgtttc1020
cctcatcctc ggctcccaca caggtgacag acccagcaga tagcttctct ctgggaaagg1080
ttggatgctg ccttacatcc ccttctagcc ctcctcccat ccacacaca aggcacccac1140
ccacaccagg teggettgtt teteacatgt agggagagag gggagaccaa cccetttgtg1200
tottttgaaa tacgaagaaa aatgtgtgtt caggagcatg actccagtgc tgcgctcttg1260
ggcctagttc agtctgtctt gtctcaaatc taggcatttt tgcttcaatt ttatttttt1320
taaaacattt ttttgggtgt cccgttggta ttggaataat ttggctaaca ttggtaaaag1380
gtaagggggt taaaatataa ggtaatttt
```

- (2) INFORMATION ON SEQ ID NO. 40:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1084 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```
ggaatcttta agcaatcata cggggaaaaa gggcccatca ccttcaaagg agccacaatt 60
agacteetea acagacatga ttgaggetgg aagataaggg aatggtatet tetteaaage 120
cgaaagaata ggaccacacc tgccaggatt tggttgttta aatataaatc tgatcacccc 180
cctgcttaga acccttctgc tttctattac ccctcattta aaatgtaaac tcttcacctt 240
ggtttatgag aactggttct tgccttcccc ttgaacctca ttaaatggtg atttcttgct 300
aagetecage cegagtggte teeteteage ttetaatttt gtgetettte etgecetttt 360
cctgggcctt ctcagctctc caccccacc actcttgact caggtggtgt ccttcttcct 420
caagtottga caattooogg goodttoagt cootgagoag totacttotg tgtotgtoac 480
cacatettgt etttteeest cattgeattt attgeagttt atatatatge taettttaet 540
tgttcatttc tgtctcccct accaggctgt aaatgagggc agaaaccttg tttgttttat 600
tcaccatcat gtaccaagtg cttggcacat agtgggcctt cattaaatgt ttgttgaata 660
aaagagggaa gaaggcaagc caaccttagc tacaatccta ccttttgata aaatgttcct 720
tttgacaata tacacggatt attatttgta ctttgttttt ccatgtgttt tgcttttatc 780
cactggcatt tttagctcct tgaagacata tcatgtgtga gataacttcc ttcacatctc 840
ccatggtccc tagcaaaatg ctaggcctgt agtagtcaag gtgctcaata aatatttgtt 900
tgggtggttt gtgagccttg ctgccaagtc ctgcctttgg gtcgacatag tatggaagta 960
tttqagagag agaacctttc cactcccact gccaggattt tgtattgcca tcgggtgcca1020
aaaa
                                                              1084
```

- (2) INFORMATION ON SEQ ID NO. 41:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2860 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

teetggetga ttetttteet ggeagtteee ettatgaggg ttacaactat ggeteetttg 60 agaatgtttc tggatctacc gatggtctgg ttgacagcgc tggcactggg gacctctctg 120 acggttacca gggccgctcc tttgaaccgg taggtactcg gccccgagtg gactccatga 180 gctctgtgga ggaggatgac tacgacacat tgaccgacat cgattccgac aagaatgtca 240 ttcgcaccaa gcaatacctc tatgtggctg acctggcacg gaaggacaag cgtgttctgc 300 ggaaaaagta ccagatctac ttctggaaca ttgccaccat tgctgtcttc tatgcccttc 360 ctgtggtgca gctggtgatc acctaccaga cggtggtgaa tgtcacaggg aatcaggaca 420 tetgetaeta caactteete tgegeecaee caetgggeaa teteagegee tteaacaaea 480 tectcageaa cetggggtae atectgetgg ggetgetttt eetgeteate atectgeaac 540 gggagatcaa ccacaaccgg gccctgctgc gcaatgacct ctgtgccctg gaatgtggga 600 tccccaaaca ctttgggctt ttctacgcca tgggcacage cctgatgatg gaggggctgc 660 tcagtgcttg cgatcatgtg tgccccaact ataccaattt ccagtttgac acatcgttca 720 tgtacatgat cgccggactc tgcatgctga agctctacca gaagcggcac-ccggacatca 780 acgccagcgc ctacagtgcc tacgcctgcc tggccattgt catcttcttc tctgtgctgg 840 gcgtggtctt tggcaaaggg aacacggcgt tctggatcgt cttctccatc attcacatca 900 togccaccot getectcage acgcagetet attacatggg coggtggaaa ctggactcgg 960 ggatcttccg ccgcatcctc cacgtgctct acacagactg catccggcag tgcagcgggc1020 cgctctacgt ggaccgcatg gtgctgctgg tcatgggcaa cgtcatcaac tggtcgctgg1080 ctgcctatgg gcttatcatg cgccccaatg atttcgcttc ctacttgttg gccattggcall40

tctqcaacct gctcctttac ttcgccttct acatcatcat gaagctccgg agtggggaga1200 ggatcaaget cateceeetg etetgeateg tttgeacete egtggtetgg ggettegege1260 tettettett ettecaggga eteageacet ggeagaaaac eeetgeagag tegagggage1320 acaaccqqqa ctgcatcctc ctcqacttct ttqacqacca cqacatctqq cacttcctct1380 cctccatcqc catgttcggg tccttcctgg tgttgctgac actggatgac gacctggata1440 ctgtgcagcg ggacaagatc tatgtcttct agcaggagct gggcccttcg cttcacctca1500 aggggcctg agctcctttg tgtcatagac cggtcactct gtcgtgctgt ggggatgagt1560 cccagcaccg ctgcccagca ctggatggca gcaggacagc caggtctagc ttaggcttqq1620 cctgggacag ccatggggtg gcatggaacc ttgcagctgc cctctgccga ggagcaggcc1680 tgctcccctg ggacccccag atgttggcca aattgctgct ttcttctcag tgttggggcc1740 ttccatgggc ccctgtcctt tggctctcca tttgtccctt tgcaagagga aggatggaag1800 qqacaccete eccattteat geettgeatt ttgeeegtee teeteeceae aatgeeecag1860 cctgggacct aaggestett tttestessa tastessact ccagggesta gtetggggss1920 tgaatctctg tcctgtatca gggccccagt tctctttggg ctgtccctgg ctgccatcac1980 tgcccattcc agtcagccag gatggatggg ggtatgagat tttggggggtt ggccagctgg2040 tgccagactt ttggtgctaa ggcctgcaag gggcctgggg cagtgcgtat tctcttccct2100 ctgacctgtg ctcagggctg gctctttagc aatgcgctca gcccaatttg agaaccgcct2160 totgattcaa gaggotgaat toagaggtoa cotottoato coatcagoto coagactgat2220 qccagcacca ggactggagg gagaagegee teacceette cetteettet ttecaggece2280 ttagtcttgc caaaccccag ctggtggcct ttcagtgcca ttgacactgc ccaagaatgt2340 ccaggggcaa aggagggatg atacagagtt cagcccgttc tgcctccata gctgtgggca2400 ccccagtgcc taccttagaa aggggcttca ggaagggatg tgctgtttcc ctctacgtgc2460 ccagtcctag cctcgctcta ggacccaggg ctggcttcta agtttccgtc cagtcttcag2520 gcaagttctg tgttagtcat gcacacacat acctatgaaa ccttggagtt tacaaagaat2580 tgccccagct ctgggcaccc tggccaccct ggtccttgga tccccttcgt cccacctggt2640 ccaccccaga tgctgaggat gggggagctc aggcggggcc tctgctttgg ggatgggaat2700 gtgtttttct cccaaacttg tttttatagc tctgcttgaa gggctgggag atgaggtggg2760 totggatott ttotcagago gtotccatgo tatggttgca tttccgtttt ctatgaatga2820 atttgcattc aataaacaac cagactcaga taaaaaaaaa

(2) INFORMATION ON SEQ ID NO. 42:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2137 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

		•				
gtccgctttc	gtctccgtcc	: tgctgccgtt	accgccgctg	ctgccgccgc	ttgcgtcccc	60
cgctccggtc	: tgtggtgcag	, ccgggaccca	ggaccatgto	: tctgtctcac	tcagaggaga	120
tgcaccggct	. cacggaaaat	: gtctataaga	ı ccatcatgga	gcagttcaac	: cctagcctcc	180
ggaacttcat	cgccatgggg	r aagaattaco	, agaaggcact	ggcaggtgtg	acgtatgcag	240
	· ceeegacgee	yy.qaaqa	liquudaaact	. aaccaacaaa	20002000-	200
auguac,	. cggagacget	Cicicodaga	taactaaaat	CCacaddcad	atcosesses	360
-900990090	. autyczyaay	Lucuttacaca	accadetact	tacqcaqctq	737737377	420
-99-90-990	. ccccaggtat	cryayiqciq	coctoaaoaa	ataccadact	Caccaaaaaa	400
geauaggege	, egeceeggae	aayigicagg	ctgagetgaa	. gaagettegg	Aagaagaga	540
agggcagcaa	gaaceeeag	aagtactcgg	acaaqqaqct	gcagtacatc	gacgccatca	600
geageaagea	gggcgagcig	yayaattacg	tgtccgacgg	ctacaadacc	acactascaa	660
aggagagaag	gagaaaaaga	Liceinggigg	agaagcagtg	Caccataacc	aagaactccc	720
-gg-ccacca	ccccaagggc	aayyagctgc	rggcgcagaa	actaccacta	taacaacaaa	700
cecycycega	ccccagcaag	accccggage	gcgcggtgca	geteatgeag	Caddtagaga	040
geaacggege	Cacccccccc	ayeyecetgt	coocciccaa	gtodaacctd	Ct Catttaca	$\alpha \alpha \alpha$
4000046666	ggggccaag	CCCCCGGGG	tucccccaa	actadeaced	ttcataaaa	0.60
49acgcccgc	ccaggagagc	acacccatca	tgaacggcgt	Cacadaccca	materona and	020
accacageee	gryggergae	Cycaaqqctq	cccadcccaa	atccctatct	CCtccccc+1	000
	geceagegae	Luciaciona	acacactccc	Catacacaaa	2000ta2001	1 4 0
- under a cond	ccatgctatt	accyayaaca	agactctgcc	Ecoctogado	tccateggaag1	200
	gegeaatgge	cycacycygg	tuaauuccar	CETCECCCSC	~ ~ + ~ ~ + ~ ~ ~ ~ 1	200
	ceceegage	LLCaaggagg	utuacetear	taccctacta	atacetes 1	220
	ceggeactat	ggagagagtq	agaagaccaa	gatgcggggc	t cattte	200
	cogggccccg	gacaycyaty	ucautuacau	actacacata	agect gas and	440
	cagcagcacg	ggcaacctcc	tuuacaadda	Caacctaacc	atcccc1	EAA
gaccacgg	cyccyccicc	Cyddocttoo	ccaccaaaa	aaccaacaac	ttc33cc3cc1	ECO
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	-9-999-9		cccadaacct	ggatgactat	CC2CCCCC+1	620
gageag	cyccyarycy	yaaytqqcca	gattctgage	CCCCtcacta	mamttamant1	C O O
TOTALGUE	acgiccage	yaayccqaca	utuaccaaco	acaddtetae	CCCCCtcct-1	7 4 0
agacgacggc	cacacccyca	grycryccca	tctaataact	Eccccaccc	ttccccatata1	0 0 0
300030000	courcatery	rguguludulg	tutadadaac	atccadaccc	COCC+CC++1	0.60
900000	accegagece	gycciqqact	quatcccadc	Tattetagge	20000000001	000
-2-2-33333	geaggeeeee	yaayyycyay	acccagtage	Eddactaccc	20000tc21	$\alpha \alpha \alpha \cdot$
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	rgagggcaca	-gcccccqqt	Cacatoocca	tagaacctta	aatacccata?	\wedge \wedge \wedge
	ggacacttgg	ccayctygtg	uctuddadda	gagectgget	gccctgctgc2;	100
ttctcctgcc	taataaacag	gcttctccta	caaaaaa	J J 0 0 9 9 0 C	guerryctycz,	137
	-		•		4.	13/

(2) INFORMATION ON SEQ ID NO. 43:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2410 base pairs

 - (B) TYPE: Nucleic acid(C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

	ttgagcagac	acaggtgcag	, gcagtggtga	ctctacaggo	cctgctattc	cgggcccttt	60
	cycaacyccy	tggcaacaat	: aaaattttga	cqtaqccatc	: ctccatttgg	aagtetagta	120
	gerggerege	cytygaaatg	accctgttt	tatttccaga	: attacctctq	ggtttägaga	180
	agiggitte	aaacgagtgt	. gggtaaaaaa	. aattacctga	ggtacttgtc	agagtcgcag	240
	acticiaggi	cccacccage	tctcatcaat	cagtttagtg	agggtggtgc	ccaggactct	300
	gattttaaac	atacccctag	aaagattctg	atacaggtag	aggtgagaag	ccctaattta	360
	gaggcagccc	ggeeteeett	catggtggga	ccagggccag	' cagggaatgt	Caggggggacc	420
	CCCGacccc	accycgaett	ctggcttgca	gagggtggcc	cqqqaqqaqa	taataaaaa	480
	ayctcaacag	cgggaaggtg	atgtacgcct	tctgcagagt	gaaggacccc	aactictiquac	540
	tycccaaatt	tgteeteate	aactggacag	gcgagggcgt	gaacgatgtg	COGGAGGGGGG	600
	cctgcgccag	ccacgccage	accatggcca	gcttcctqaa	gggggccat	gtgaccatca	660
	acycacygge	cgaggaggat	grggagcctg	agtqcatcat	ggagaaggtg	gccaaggett	720
	caygraccaa	ctacagettt	cacaaggaga	gtggccgctt	ccaggacgtg	ggaccccagg	780
	ceccageggg	ctctgtgtac	cagaagacca	atgccgtgtc	tgagattaaa	agggttggta	840
	aayacagctt	ctgggccaaa	gcagagaagg	aggaggagaa	ccatcaacta	gaggaaaagc	900
	ggcgggccga	ggaggcacag	cggcagtgga	gcaggagcgc	caggagcata	agtgcgtgag	960
	gergeaegee	gggagcagcg	ctatcaggag	cagggtggcg	aggccagccc	ccagaggacgl	020
	Çgggagcagc	agcaagaagt	ggtttcaagg	aaccgaaatg	agcaggagtc	taccatacac1	080
	ccgagggaga	ttttcaagca	gaaggagagg	gccatgtcca	ccacctccat	ctccagtcctl	140
	caycetggca	agcigaggag	ccccttcctg	cagaagcagc	tcacccaacc	agagacccac1	200
	tttggcagag	agccagctgc	tgccatctca	aggcccaggg	cagatetece	tactaaggag1	260
	ccggcgccca	geacteetee	atgtctggtg	caggcagaag	aggaggctgt	gtatgaggaa1	320
	ccccagage	aggagaccit	ctacgagcag	ccccactgg	tocaocaoca	aggtgctggc1	380
	ccigagcaca	Ligaccacca	cattcagggc	caggggctca	gtgggcaagg	gctctgtgcc1	440
	cgcgccccgc	acgactacca	ggcagccgac	gacacagaga	tctcctttga	CCCCgagaac1	500
	ctcatcacgg	gcatcgaggt	gatcgacgaa	ggctggtggc	gtggctatgg	accagatage1	560
	cattttggta	rgrieddige	caactacgtg	gageteattq	agtgaggctg	agggcacatc1	620
	tigecettee	cccccagae	atggcttcct	tattgctgga	agaggaggcc	taggaattga1	680
	catteageac	tetteeagga	ataggacccc	cagtgaggat.	gaggeeteag	ggetecetec1	740
•	ggcccggcag	acteageetg	tcaccccaaa	tgcagcaatg	gcctggtgat	tcccacacat1	ลดด
	cccccccca	receeegaee	ctcccagaca	gcttggctct	tacccctaac	aggatactgal	860
•	gccaagcccc	geetgtggee	aagccctgag	tggccactgc	caagctgcgg	ggaagggtcc1	920
	cgagcagggg	catcugggag	gctctggctg	ccttctgcat	ttatttgcct	tttttctttt1	980
	cecergee	CLAAGGGGTG	grggccacca	ctgtttagaa	tgacccttgg	gaacagtgaa2	040
١	Julian	cyciccage	agagtttgtg	accaaagtca	gagtggatca	taataattta2	100
`	gcagcaggga	accidictig	ttggagcctg	ctctgtgctc	cccactccat	ttctctgtcc2	160
•	Jeeegeeegg	gctatgggaa	grggggargc	agatggccaa	gctcccaccc	tgggtattca2:	220 i
•	aaacyycay	acacaacatg	ttcctccacg	cggctcactc	gatgcctgca	ggcccagta2	280
١	gegeeteaa	ctgattetga	cttcaggaaa	agtaacacag	agtggccttg'	acctattatc2	340
,	cocciaci	ttctgtccca	gctcatccgt	gtctctgaag	aacaaatato	cttttggacc2	400
č	aaaaaaaa				,		410
						· -	

(2) INFORMATION ON SEQ ID NO. 44:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2333 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```
tgaaaaatgc ggacagtata ttcagaaagg ctattccaag ctcaagatat ataattgtga
actagaaaat gtagcagaat ttgagggcct gacagacttc tcagatacgt tcaagttgta 120
ccgaggcaag tcggatgaaa atgaagatcc ttctgtggtt ggagagttta agggctcctt 180
teggatetae cetetgeegg atgaceceag egtgeeagee eeteceagae agttteggga 240
attacctgac agcgtcccac aggaatgcac ggttaggatt tacattgttc gaggcttaga 300
gctccagccc caggacaaca atggcctgtg tgacccttac ataaaaataa cactgggcaa 360
aaaagtcatt gaagaccgag atcactacat tcccaacact ctcaacccag tctttggcag 420
gatgtacgaa ctgagctgct acttacctca agaaaaagac ctgaaaattt ctgtctatga 480
ttatgacacc tttacccggg atgaaaagt aggagaaaca attattgatc tggaaaaccg 540
attectttee egetttgggt eccaetgegg cataceagag gagtactgtg tttetggagt 600
caatacctgg cgagatcaac tgagaccaac acagctgctt caaaatgtcg ccagattcaa 660
aggetteeca caacceatee ttteegaaga tgggagtaga ateagatatg gaggaegaga 720
ctacagettg gatgaatttg aagccaacaa aatcetgeac cagcaceteg gggeeeetga 780
agageggett getetteaca teeteaggae teaggggetg gteeetgage aegtggaaac 840
aaggactttg cacagcacct tecageceaa cattteecag ggaaaactte agatgtgggt 900
ggatgttttc cccaagagtt tggggccacc aggccctcct ttcaacatca caccccggaa 960
agccaagaaa tactacctgc gtgtgatcat ctggaacacc aaggacgtta tcttggacga1020
gaaaagcatc acaggagagg aaatgagtga catctacgtc aaaggctgga ttcctggcaa1080
tgaagaaaac aaacagaaaa cagatgtcca ttacagatct ttggatggtg aagggaattt1140
taactggcga tttgttttcc cgtttgacta ccttccagcc gaacaactct gtatcgttgc1200
gaaaaaagag catttctgga gtattgacca aacggaattt cgaatcccac ccaggctgat1260
cattcagata tgggacaatg acaagttttc tctggatgac tacttgggtt tcctagaact1320
tgacttgcgt cacacgatca ttcctgcaaa atcaccagag aaatgcaggt tggacatgat1380
teeggaeete aaageeatga acceeettaa ageeaagaea geeteeetet ttgageagaa1440
gtccatgaaa ggatggtggc catgctacgc agagaaagat ggcgcccgcg taatggctgg1500
gaaagtggag atgacattgg aaatcctcaa cgagaaggag gccgacgaga ggccagccgg1560
gaaggggggg gacgaaccca acatgaaccc caagctggac ttaccaaatc gaccagaaac1620
ctccttcctc tggttcacca acccatgcaa gaccatgaag ttcatcgtgt ggcgccgctt1680
taagtgggtc atcatcggct tgctgttcct gcttatcctg ctgctcttcg tggccgtgct1740
cctctactct ttgccgaact atttgtcaat gaagattgta aagccaaatg tgtaacaaag1800
gcaaaggctt catttcaaga gtcatccagc aatgagagaa tcctgcctct gtagaccaac1860
atccagtgtg attttgtgtc tgagaccaca ccccagtagc aggttacgcc atgtcaccga1920
gccccattga ttcccagagg gtcttagtcc tggaaagtca ggccaacaag caacgtttgc1980
atcatgttat ctcttaagta ttaaaagttt tattttctaa agtttaaatc atgtttttca2040
aaatattttt caaggtggct ggttccattt aaaaatcatc tttttatatg tgtcttcggt2100
tctagacttc agcttttgga aattgctaaa tagaattcaa aaatctctgc atcctgaggt2160
gatatacttc atatttgtaa tcaactgaaa gagctgtgca ttataaaatc agttagaata2220
gttagaacaa ttcttattta tgcccacaac cattgctata ttttgtatgg atgtcataaa2280
agtotattta acctotgtaa tgaaactaaa taaaaatgtt toacotttaa aac
```

- (2) INFORMATION ON SEQ ID NO. 45:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1612 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
gtottotttt ttttotttt tttttttt ttttttttc cotgtggaag tgottttatt 60
agcagtaagg ctgatcgtac aaaaaattct cagagcttca taggacaagg tagtacaagt 120
atggatgata caggactgag gaacggggga cggctcaaaa gaaatcaaca tcgtctgggg 180
catccaggtc ccgatattcc acaatggccc ttgggtctcc acgaaccatc ctgttgcgag 240
gtttcccagg ataacctccc tggcctcgga aggcatcata gttccctcga ccagcaccat 300
acggggcatg ggggtatgga gggcctcctg tggggactgc agggcggaca gcaccagctc 360
catageceaa gateggggge eggggetgae catagggeat eaggeeetgg ggagtetggt 420
gtgggtaggg gagtcctggg gtcaaacctg gggggagtat ctgggcgggc ccaggtggct 480
gggctggctt gatctcaggc agagctgggc gcttagcatc agtgaggaag ttgttaaaaa 540
acgcgacttc ctttttcact tecteaattt tetetgeatg ettgttgaag atatgtttge 600
gcacaaactc aggacccttg aatttcttgc cactgagagg acacagccac ttatccttgc 660
ccagttcctg cgtgttggag gtgacgaact tctccacttc ctgctctggg tctttgcgcc 720
ccatcttctg ggcctcttcc tctgagagtg actcccgcac actcagcaac ggcgtgagct 780
tetecteaaa agtettetge cacteeagea etteecegtg aetgatgegg ttgggtggea 840
tgggcccccg aacgtggatg atcccacage gattgggcat ctcgtcctcg ttggggtact 900
cacaggtgtt gtaataatcc aaggaatgca cgatgcgcag gtaaaggagg agcttgtcca 960
agacettaat caacttetea teeegeteea egitgatete tgeegggite cetteettag1020
gaggeteete aggaggageg eeceegetge teeceageag eteeteetee teggegetta1080
cttcctcgat caggtagtcg gtgatattct tcaagatcgg gttttgcgag ggcaggctcg1140
tgggcagggg aggcgtccct ggttctgagg cccaaagctg tgtcctgtca tccagcgtgt1200
ggatcagett ggeegeeage ttgatgtegt tgegeaeaat etgettgtge tgggtgatge1260
cgttgatgtt gcgaacgcgc cgggtcaggt ccctgttcac accagggctc agctcacact1320
cccggagacg gatgttctgc aggttccaac agatctcttt aatgttaaca ctgcggtcgal380
aggtcaccca gccacgacgg aaaaacctcc tctctggctg gggctctgag agcgccaccc1440
gcataaagcc tgggtacctt ttacaaaggg agatgatctc ggcccgggag atgttgggcq1500
cgatgttgcg catgaagagg gagcaggtct tatgcagcgg ccgcqgcttg cactccaqcc1560
coggogete cttgggctte teccattett ettecttggg etteteette te
```

- (2) INFORMATION ON SEQ ID NO. 46:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1106 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 - ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```
gaaagetetg gettteagge tataggaaga geagaagatg atgeeagaag ttgetgggtt 60
aaaaccageg agtccacceg teettaccag eteetcagaa ggeggagace gaccetgata 120
acttaccgga tatttcgtca cagaagacac aaagacacat ccagcgggga ccacctcacc 180
tgcagattag acccccaagc caaagacctg aaggatggga cccaggagga ggccacaaaa 240
aggcaagaag cccctgtgga tccccgcccg gaaggagatc cgcagaggac agtcatcagc 300
tgqaqqqag cggtgatcga gcctgagcag ggcaccgagc tcccttcaag aaqaqcaqaa 360
gtgcccacca agcctcccct gccaccggcc aggacacagg gcacaccagt gcatctgaac 420
tatcgccaga agggcgtgat tgacgtcttc ctgcatgcat ggaaaggata ccgcaagttt 480
gcatggggcc atgacgagct gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc 540
ggtctcacac tgatcgacgc gctggacacc atgtggatct tgggtctgag gaaagaattt 600
gaggaagcca ggaagtgggt gtcgaagaag ttacactttg aaaaggacgt ggacgtcaac 660
ctgtttgaga gcacgatccg catcctgggg gggctcctga gtgcctacca cctgtctggg 720
gacageetet teetgaggaa agetgaggat tttggaaate ggetaatgee tgeetteaga 780
acaccatcca agattcctta ctcggatgtg aacatcggta ctggagttgc ccacccgcca 840
cggtggacct ccgacagcac tgtggccgag gtgaccagca ttcagctgga gttccgggag 900
ctctcccgtc tcacagggga taagaagttt caggaggcag tggagaaggt gacacagcac 960
atccacggcc tgtctgggaa gaaggatggg ctggtgccca tgttcatcaa tacccacagt1020
gggcctgttt cacccacctg gggcgtattt cacggtgggg cgccaggggc cgacagctta1080
ttattgagtt acctgtttga aaggca
```

(2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1370 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```
geggtggega ggggegtaae ggttgttgta gteeggeeee eteetggetg gteeageeae
attaaccggc aggatgtcgg aggtgcggct gccaccgcta cgcgccctgg acgactttgt 120
tetggggteg gegegtetgg eggeteegga tecatgegae eegeagegat ggtgceaecg 180
egicateaac aaceteetet actaecaaac caactaeett etetgetteg geateggeet 240
egetetegee gggtaegtge ggeeacttea taegeteetg agegegetgg tagtggeggt 300
ggccctcggc gtgctggtgt gggcagctga gacccgcgca ctgtgcgccg ctgccqccgc 360
agccaccetg cagcetgeet ggccgcagtg cttgccgtcg gcctcctggt gctctgggtc 420
gegggeggeg ettgeacett cetgtteage ategeeggge eggtgettet gateetggtg 480
cacgcctcgt tgcgcctgcg caaccttaag aacaagattg agaacaagat cgagagcatt 540
ggtctcaagc ggacgccaat gggcctgcta ctagaggcac tgggacaaga gcaggaggct 600
ggatectagg eccetgggat etgtacecag gacetggaga ataceaece acceecagee 660
cataattggg acccagagcc ctttcccagc acttaaaaca ggagcctaga gccccctgcc 720
caaacaaaac aggacatctg tgaccgccct acccccacgc cagccccaaa ctaagatatc 780
cctcacaccc agcccccatt acctagggac aagagtcttc cccagccttg aacctaggac 840
caagagccac ctacatccag ccccaaaact ggggcttcag gccagagcat ccatggccaa 900
tttcaaattg tgaacccaga gacactccca tccacccttc tccatgctca tccccaaact 960
ggggcctgga gcaaggcact ctcaaatctt gaaccctgga ccaaagcttt tccagacccc1020
accetacett ccaacccagg tcaagacatt gccaaatett gaactcagaa cccaagtgtt1080
ccatgcccct gtgtggatgg agtcgggtat cctgactgtt ggacccctgg tccaqqtgat1140
cccgaccete accagtecea tttgcctcce tccagetetg cttaggeatt ttgcccetcal200
ccccaatgtt ccacaccatc gacaaccaag gggtgaggtg gggacaggcc tcagcaggga1260
atggggcgta tatgttagtg ttgctgcaac aataaagcct gttgcatctc tcatgccaaa1320
aaaaaaaaa aagtcgaccg gccgcaaata tagtagtagt agtcgtccgc
```

- (2) INFORMATION ON SEQ ID NO. 48:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 617 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

ctcgtagttt attaaatgat gtacaatttg gccagtttgg agatgacca aaggaggaag 60 taatggttct ggagagatc ttactggcag accatcaagg ttgatttaca ggtagaacat120 ccataccagt tcctactaaa atatgcaaag caactcaaag gtgataaaaa caaaattcaa180 aagttggttc aaatggcatg gacatttgta aatgacagtc tctgcaccac cttgtcactg240 cagtgggaac cagagatcat agcagtagca gtgatgtatc tcgcaggacg tttgtgcaaa300 tttgaaatac aagaatggac ctccaaaccc atgtatagga gatggtgga gcagtttgtt360 caaggaaaac aacagatgcc tcatcacacc atctcacac ccccatcagc tgcaacagc cccaatctcct480 gagcctcca agccgacc tgggccctgt ggttgctggg cctccaaa accaagaggg540 aaggttgtac agccgaacc cgtggagcaa tgcctgtct ggcctcaaa accaaaataa600 aactgggtca ctttaaa

- (2) INFORMATION ON SEQ ID NO. 49:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1899 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```
tgtgtgaggc ccaacagcgg aatcatcgat gcaggggcct gaattaatgt atctgtgatg
ttacagcctt tcgattatga tcccaatgag aaaagtaaac acaggttatg gttcagtcta 120
tgtttgctcc aactgacact tcagatatgg aagcagtatg gaaggaggca aaaccggaag 180
accttatgga ttcaaaactt agatgtgtgt ttgaattgcc agcagagaat gataaaccac 240
atgatgtaga aataaataaa attatatcca caactgcatc aaagacagaa acaccaatag 300
tgtctaagtc tctgagttct tctttggatg acaccgaagt taagaaggtt atggaagaat 360
gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag ttcaaggaag 420
aagatggact gcggatgagg aagacagtgc agagcaacag ccccatttca gcattagccc 480
caactgggaa ggaagaaggc cttagcaccc ggctcttggc tctggtggtt ttgttcttta 540
tegttggtgt aattattggg aagattgeet tgtagaggta geatgeacag gatggtaaat 600
tggattggtg gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 660
aattaatgta tgatgacatc tcacaggtct tgcctttaaa ttacccctcc ctgcacacac 720
atacacagat acacacaca aaatataatg taacgatctt ttagaaagtt aaaaatgtat 780
agtaactgat tgagggggaa aagaatgatc tttattaatg acaagggaaa ccatgagtaa 840
tgccacaatg gcatattgta aatgtcattt taaacattgg taggccttgg tacatgatgc 900
tggattacct ctcttaaaat gacacccttc ctcgcctgtt ggtgctggcc cttggggagc 960
tggagcccag catgctgggg agtgcggtca gctccacaca gtagtcccca cgtggcccac1020
teceggeeca ggetgettte egtgtettea gttetgteea agecateage teettqqqac1080
tgatgaacag agtcagaagc ccaaaggaat tgcactgtgg cagcatcaga cqtactcgtc1140
ataagtgaga ggcgtgtgtt gactgattga cccagcgctt tggaaataaa tggcagtgct1200
ttgttcactt aaagggacca agctaaattt gtattggttc atgtagtgaa gtcaaactgt1260
tattcagaga tgtttaatgc atatttaact tatttaatgt atttcatctc atgttttctt1320
attgtcacaa gagtacagtt aatgctgcgt gctgctgaac tctgttgggt gaactggtat1380
tgctgctgga gggctgtggg ctcctctgtc tctggagagt ctggtcatgt ggaggtgggg1440
tttattggga tgctggagaa gagctgccag gaagtgtttt ttctgggtca gtaaataaca1500
actgtcatag ggagggaaat tctcagtagt gacagtcaac tctaggttac cttttttaat1560
gaagagtagt cagtcttcta gattgttctt ataccacctc tcaaccatta ctcacacttc1620
cagcgcccag gtccaagtct gagcctgacc tccccttggg gacctagcct ggagtcagga1680
caaatggatc gggctgcaga gggttagaag cgagggcacc agcagttgtg ggtggggagc1740
aagggaagag agaaactctt cagcgaatcc ttctagtact agttgagagt ttgactgtga1800
attaatttta tgccataaaa gaccaaccca gttctgtttg actatgtagc atcttgaaaa1860
gaaaaattat aataaagccc caaaattaag aaataaaaa
                                                                 1899
```

(2) INFORMATION ON SEQ ID NO. 50:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1398 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```
agaatgtcgg gcggtgctgc gaggcccaag cccgggccgg ggccgcctcc ctcaacgcct 60
cccttqacqq cctccacaac gcactcttcg ccactcagcq cagcttggag cagcaccagc 120
ggctcttcca cagcctcttt gggaacttcc aagggctcat ggaagccaac gtcagcctgg 180
acctggggaa gctgcagacc atgctgagca ggaaagggaa gaagcagcag aaagacctgg 240
aagctccccg gaagagggac aagaaggaag cggagccttt ggtggacata cgggtcacag 300
ggcctgtgcc aggtgccttg ggcgcggcgc tctgggaggc aggatcccct gtggccttct 360
atgccagett ttcagaaggg acggctgccc tgcagacagt gaagttcaac accacataca 420
tcaacattgg cagcagctac ttccctgaac atggctactt ccgagcccct gagcgtggtg 480
totacctgtt tgcagtgagc gttgaatttg gcccagggcc aggcaccggg cagctggtgt 540
ttggaggtca ccatcggact ccagtctgta ccactgggca ggggagtgga agcacagcaa 600
cggtctttgc catggctgag ctgcagaagg gtgagcgagt atggtttgag ttaacccagg 660
gatcaataac aaagagaagc ctgtcgggca ctgcatttgg gggcttcctg atgtttaaga 720
cctgaaccc agccccaatc tgatcagaca tcatggactc gcccagetct cctcggcctg 780
gggctctggc caaggatggg ctggaggtca ttcagttggt ctgtctcttc cctggaaacc 840
ttctgcaaag atggtgtgt gtacgtggct tccctgtaac cacatggggc ttggccattt 900
ctccatgatg agaaggactg gaatgettet eegggeagga catggteeta ggaageetga 960
accttggctt ggcatgcctt ctcagacagc acggcctggg ctccaactct tcaccacacc1020
ctgtattcta caacttcttt ggtgttttgc tcctcctgtg gttggaaact tctgtacaac1080
actttaaact tttctcttgc ttcctcttct cttctccctt atcgtatgat agaaagacat1140
tcttccccag gaggaatgtt taaaatggag gcaacatttt ggccaacatt ggaaagcact1200
agagggcaat gggattaaac caacctgctt ggtctctatt agtcagtaat gaagacgaca1260
gcctggccaa ccaagggaaa ggaaattagt atctttagtt tcagtcattc cttgtagggg1320
tatgggtttt agcttgtggc ccccaccgaa aagattcatc ttggattgtt aatgcctatt1380
                                                                  1398
attccccaca ttaagggg
```

(2) INFORMATION ON SEQ ID NO. 51:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1340 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```
tttggcatca tttacaattt catagaatta ctgtgaaggc ctttctagtt gagatgttgg 60
ggtatttggg attctaattg ttaaccccag aagaaggtaa tttagcttgt atttatttaa 120
aacccattta qccttttact tatatctggt agaattccag tgatcatcct aataaggtat 180
atttcagaat aattttttt tccttcagaa taacttagaa tcagatgcta taagggctcc 240
taggagcagt gtgaaatttc cgtaaagata aatttgaatg ttgtaaccaa gtttatätta 300
aaccaagagg ccatttccaa tatgattttt tgtttctttt taacttgtta agtccctaag 360
agattacatg ctagggettg agtcatttct attgtagata atgatggeec acacagteae 420
cttcaactat ccacataagc taggctttcc gcttttgcca cggacagtgt gaccaagata 480
tttccagagt aaataaccca ccacaacctt ggtaattcct cttttcttct taagctccag 540
gaagegaaag cagaaggact etttteagae tgeeetetgt ageetacatt geagetttee 600
aaaacaggca gctagcactg ggaaagccca tgtggtgacc ccatattttt ctgaggttct 660
tcttttccat ggtgttactt tattatcaga aagtaaattc agaaaacagg tcttgccctt 720
agcagacaag aaccacacca gtttcttgta aaggtaacgg atacattggg attcaggagt 780
gacacagagg tccagcccca gaacttgtaa ggattttgtt tgaacactga gcagatgcct 840
cctccctgcc acccatcaca ctagttaggg ctggccatga attctatgcc agagtcactc 900
ttgccttcac agagtcctcc ttgacacccc tgacttaatg atagttgctg ttttggagta1020
gaattgatca ggtttaagtc atcctgctca ggttgggcat agtggctcat gcctgtaatc1080
tcagcacttt gggaagccaa agtgggagga ttgcttgagc ccaggagttc caaaccatcc1140
tgggcaacag agggagaccc tgtctctacc aagaaaaaaa aaaaaaaaa aaagttaaaa1200
aaacaattag ctggacctgg tggtgcacac tcagtaggct gaggtgaaag gattcctttal260
acatgggaga ctgaagatgc agtgagccat gaatcagcaa ctgcacacca gtatgagaga1320
aaaagtggaa ccctatcaca
```

- (2) INFORMATION ON SEQ ID NO. 52:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

atcagcacat caattgcagc attgtggcta ccagggggtc aggatgcggg cggtggagcc 60 ctctggcctt tgtgtggtag ccgaggactc tgtgtcagcg accgttttcc gggaaacttc120 cgggcgagac tcacatcttg gaaattcaaa tactcaatag ctctcgaatt ctaggaatct180 tgagaagagg cctggattaa ggattcagac gtgggccctc agatggctat ggcattgctg240 gttctaccaa cgtgacaggt gatcaagtta agaagctgga cgtcctctcc aacgacctgg300 gtatggaaca ggtta

- (2) INFORMATION ON SEQ ID NO. 53:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1162 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```
cggctcgagc ggctcgagat tcgaggtcgt ggtggtcttg gaagagcgtc gagggggccg
tggacgtgga atgggccgag gagatggatt tgattctcgt ggcaaacgtg aatttgatag 120
gcatagtgga agtgatagat ctggcctgaa gcacgaggac aaacgtggag gtagcggatc 180
tcacaactgg ggaactgtca aagacgaatt aacagagtcc cccaaataca ttcagaaaca 240
aatatottat aattacagtg acttggatca atcaaatgtg actgaggaaa cacctgaagg 300
tgaagaacat catccagtgg cagacactga aaataaggag aatgaagttg aagaggtaaa 360
agaggagggt ccaaaagaga tgactttgga tgagtggaag gctattcaaa ataaggaccg 420
ggcaaaagta gaatttaata tccgaaaacc aaatgaaggt gctgatgggc agtggaagaa 480°
gggatttgtt cttcataaat caaagagtga agaggctcat gctgaagatt cggttatgga 540
ccatcatttc cggaagccag caaatgatat aacgtctcag ctggagatca attttggaga 600
cettggccgc ccaggacgtg gcggcagggg aggacgaggt ggacgtgggc gtggtgggcg 660
cccaaaccgt ggcagcagga ccgacaagtc aagtgcttct gctcctgatg tggatgaccc 720
agaggcattc ccagctctgg cttaactgga tgccataaga caaccctggt tcctttgtga 780
accettetgt teaaagettt tgeatgetta aggatteeaa acgaetaaga aattaaaaaa 840
aaaaagactg tcattcatac cattcacacc taaagactga attttatctg ttttaaaaat 900
gaacttctcc cgctacacag aagtaacaaa tatggtagtc agttttgtat ttagaaatgt 960
attggtagca gggatgtttt cataattttc agagattatg cattcttcat gaatactttt1020
gtattgctgc ttgcaaatat gcatttccaa acttgaaata taggtgtgaa cagtgtgtac1080
cagttaaaaa aatcacaaaa aaaaaaaatt ttaattaagg atttagaagt tcccccaatt1140
acaaactggt tttaaatatt gg
```

- (2) INFORMATION ON SEQ ID NO. 54:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1826 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

				:		
cggctcgagg	cccccgccct	gttcgccccg	cgccaccggc	ccgcgccccg	ccatggagga	60
cctggatgcc	ctgctctctg	acctggagac	taccacctcg	cacatgccaa	ggtcaggggc	120
tcccaaagag	cgccctgcgg	agcctctcac	ccctccccca	tcctatggcc	accagccaca	180
gacagggtct	ggggagtctt	caggagcctc	gggggacaag	gaccacctgt	acagcacggt	240
atgcaagcct	cggtccccaa	agcctgcagc	cccggcggcc	cctccattct	cctcttccaq	300
cggtgtcttg	ggtaccgggc	tctgtgagct	agatcggttg	cttcaggaac	ttaatgccac	360
tcagttcaac	atcacagatg	aaatcatgtc	tcagttccca	tctagcaagg	tggcttcagg	420
agagcagaag	gaggaccagt	ctgaagataa	gaaaagaccc	agcctccctt	ccagcccgtc	480
tcctggcctc	ccaaaggctt	ctgccacctc	agccactctg	gagctggata	gactgatggc	540
ctcactctct	gacttccgcg	ttcaaaacca	tcttccagcc	tctgggccaa	ctcagccacc	600
ggtggtgagc	tccacaaatg	agggctcccc	atccccacca	gagccgactg	gcaagggcag	66.0
cctagacacc	atgctggggc	tgctgcagtc	cgacctcagc	cgccggggtg	ttcccaccca	720
ggccaaaggc	ctctgtggct	cctgcaataa	acctattgct	gggcaagtgg	tgacggctct	780
gggccgcgcc	tggcaccccg	agcacttcgt	ttgcggaggc	tgttccaccg	ccctgggagg	840
cagcagcttc	ttcgagaagg	atggagcccc	cttctgcccc	gagtgctact	ttgagcgctt	900
ctcgccaaga	tgtggcttct	gcaaccagcc	catccgacac	aagatggtga	ccgccttggg	960
cactcactgg	cacccagagc	atttctgctg	cgtcagttgc	ggggagccct	tcggagatga1	1020
gggtttccac	gagcgcgagg	gccgccccta	ctgccgccgg	gacttcctgc	agctgttcgc1	.080
cccgcgctgc	cagggctgcc	agggccccat	cctggataac	tacatctcgg	cgctcagcgcl	140
gctctggcac	ccggactgtt	tcgtctgcag	ggaatgcttc	gcgcccttct	cgggaggcagi	200
ctttttcgag	caçgagggcc	gcccgttgtg	cgagaaccac	ttccacgcac	gacgcggctc1	.260
gctgtgcgcc	acgtgtggcc	tccctgtgac	cggccgctgc	gtgtcggccc	tgggtcgccg1	.320
cttccacccg	gaccacttca	catgcacctt	ctgcctgcgc	ccgctcacca	aggggtcctt1	.380
ccaggagcgc	gccggcaagc	cctactgcca	gccctgcttc	ctgaagctct	tcggctgacal	.440
gcccgctcgg	ctcgccctct	ccccggagg	ccgcgccctc	ccggaaaagc	cgggtcctcc1	1500
agaccccgag	gccttgctct	cagagcggga	ggccccaccc	actggagagc	cccgccccta1	1560
aggtactatg	agtcctcagg	ggtcaagttc	agaaacggcc	cagccagacc	taaacccaca1	620
cgcccacaaa	gtggattgca	cacagacaag	aactcccgtg	cgggcctcca	ctctattccc1	.680
acccttgagg	gagccccctt	actgggggag	ggtccttgca	attccagcga	atcggaggcc1	740
aggccaggac	gtccttgctc	cctgcaccct	cactgttctg	tgcacttttt	ctacctacatl	.800
aaacacacgc	attccacctc	aaaaaa	•	•		.826

- (2) INFORMATION ON SEQ ID NO. 55:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1114 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

gatgaagtag atgactttga ggacttcatc ttcagccact tctttggaga caaagcactg 60 aagaagaggt cagggaagaa ggacaagcac tcacagagcc caagagctgc ggggcccagg 120 gaggggcaca gcataggggg ctgacaccct gccccacagg gaatggcctt ggcctggccc 180 agcccaagat cccagcgtta tctaactcct ggagggtgga ctctgtcctg gcttgtttgg 240 tgtcctcaga tatctttcac acagtagage aaaatcacca gccctgcact gatgtcactt 300 tatgtagaaa aaggcettag etggacetge gttgeegtet atgcaaatge atgcaaatae 360 tccaggccct gggatgtggg cttgtgtttt gtcactgtga agggggagat gggagaggag 420 cctgttttgg ggtggggtct ggggaaggca atctgattct gaagctaaag agctttcatc 480 ctcttgagtg tatgtcccca tagtgggccc cttgacccac atgctgaccg gtgccttggg 540 atttgactag agttgctggc tcgaggccca gcacgaggac ttaccctggg gttttgttag 600 gtttggaagc agctgtccct agggggtgaa gtccccccc ttttttttt tttacccctg 660 cttctcccac ggcttcacct ccctatgtga actgtagact cagatcccaa taaagtgctg 720 ttgcagctat gatgctaggt ggtttctaag cacaggggac accccacacc ccctgcctga 780 atggatgggt ccatcccagg cactggtact tgccccttg ttctgtatcc ccctttgccc 840 ttgccttgcc cttccaacaa accctaggcc cttgagaagc tgatacttct ccttttgctc 900 acaqctqcct tqqccccacc cctqqqaqat qtaqcaaatt qaqtqtqqqt tttqqaqtct 960 qaqcctcagg ctcaaatcca ggccaagtga tcttgggcaa gttaatctct gggaactttg1020 qqtttcttat cctcaaaaaa qqcqatqqaa qqqctqqqqa aqtqattaaa taaaaqcaac1080 qcaagaaaaa aaaaaaaaaa aaaaaaaaaa aaaa

- (2) INFORMATION ON SEQ ID NO. 56:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1644 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 - ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```
ctcqaqccqt qcaaqtqqaa taacacgggc tgccaggccc tgcccagcca agaacgaagg 60
ccccagcaag gccttcgtga actgtgacga gaacagccgg cttgtctccc tgaccctgaa 120
cctggtgacc agggctgatg agggctggta ctggtgtgga gtgaagcagg gccacttcta 180
tggagagact gcagccgtct atgtggcagt tgaagagagg aaggcagcgg ggtcccgcga 240
tgtcagccta gcgaaggcag acgctgctcc tgatgagaag gtgctagact ctggttttcg 300
ggagattgag aacaaagcca ttcaggatcc caggcttttt gcagaggaaa aggcggtggc 360
agatacaaga gatcaagccg atgggagcag agcatctgtg gattccggca gctctgagga 420
acaaggtgga agctccagag cgctggtctc caccctggtg cccctgggcc tggtgctggc 480
agtgggagcc gtggctgtgg gggtggccag agcccggcac aggaagaacg tcgaccgagt 540
ttcaatcaga agctacagga cagacattag catgtcagac ttcgagaact ccagggaatt 600
tggagccaat gacaacatgg gagcctcttc gatcactcag gagacatccc tcggaggaaa 660
agaagagttt gttgccacca ctgagagcac cacagagacc aaagaaccca agaaggcaaa 720
aaggtcatcc aaggaggaag ccgagatggc ctacaaagac ttcctgctcc agtccagcac 780
cgtggccgcc gaggcccagg acggccccca ggaagcctag acggtgtcgc cgcctgctcc 840
ctgcacccat gacaatcacc ttcagaatca tgtcgatcct ggggccctca gctcctgggg 900
accecactee etgetetaac acctgeetag gttttteeta etgteeteag aggegtgetg 960
gtcccctcct cagtgacatc aaagcctggc ctaattgttc ctattgggga tgagggtggc1020
atgaggaggt cccacttgca acttctttct gttgagagaa cctcaggtac ggagaagaat1080
agaggteete atgggteet tgaaggaaga gggaccaggg tgggagaget gattgeagaa1140
aggagagacg tgcagcgcc ctctgcaccc ttatcatggg atgtcaacag aatttttccc1200
tocactocat coctocctoc cgtccttccc ctcttcttct ttccttccat caaaagatgt1260
atttgaattc atactagaat tcaggtgctt tgctagatgc tgtgacaggt atgccaccaal320
cactqctcac agcetttctq aggacaccag tgaaagaagc cacagetett cttggcgtat1380
ttatactcac tgagtcttaa cttttcacca ggggtgctca cctctgcccc tattgggaga1440
ggtcataaaa tgtctcgagt cctaaggcct taggggtcat gtatgatgag catacacaca1500
ggtaattata aacccacatt cttaccattt cacacataag aaaattgagg tttggaagag1560
tgaagcgttt ttctttttct ttttttttt tgagacggag gtcttcactg tcgcccaggc1620
tggagtgcag tggcgcaatc tcgg
```

(2) INFORMATION ON SEQ ID NO. 57:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2184 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

	,					
tgcagtggtc	agagtgacct	ggtataaggg	agagggcatc	accttgcccc	ctgtgctgac	60
tcctgccctt	gtgcgagggg	agtccatccc	gatccggctc	ttcctggccg	ggtatgagct	120
cacgcccacc	atgcgggaca	tcaacaagaa	gttctctgtg	cgctattacc	tcaacctggt	180
gctgatagac	gaggaggagc	ggcgctactt	caagcagcag	gaagtggtgt	tgtggcggaa	240
gggtgacatc	gtacggaaga	gcatgtccca	ccaggcggcc	atcgcctcac	agcgctttga	300
gggcaccacc	tccctgggtg	aggtgcggac	ccccagccag	ctgtctgaca	acaactgcag	360
gcagtaggcc	cccagggccg	agaagatgct	gggcacccac	ccagcacccc	catctaccaa	420
		ggcggacctt				480
		tgacttaaat				540
		tgggattctg				600
		ggaacatgag				660
		gcacgcatcc				720
		gggattctga				780
		ccggaggtag				
		tgggaagcta				
		ccttctggcc				
		cagtaatgtc				
		cagtgtcgtg				
		gaagatgagt				
		tgggctgttc				
		ccctgaagaa				
gccttgctga	gagtgaaccc	tegtetetee	tcaccctcca	tttcatttct	gggaattggg]	1320
		caaggctgtt				
		gagaccaggg				
		aggtcatctt				
		aacacatata				
		cctctacggc				
		tcccctggaa				
		aagcaggccc				
		aaagttaagg				
		ttttcctgag				
		tggagggaga				
		ggcaaggttg				
		gaacaggatc				
		aggcaagttc				
		ttcctagctg	atattctaac	tagaagcatt		
cctgtgtggc	ccttccccc	agag			2	2184

(2) INFORMATION ON SEQ ID NO. 58:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1510 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```
agcctgggaa acacagtagg gctccacctc tacaaaaaac acaaaaatta gccaggcatg
tggcgtcata gtagaattaa tcaaaagcaa gaaaatggct ggaggagctg tcttgttggc 120
aggaceteet ggaactggea agacagetet ggetetgget attgeteagg agetgggtag 180
taaggtcccc ttctgcccaa tggtggggag tgaagtttac tcaactgaga tcaagaagac 240
agaggtgctg atggagaact teegeaggge cattgggetg egaataaagg agaccaagga 300
agtttatgaa ggtgaagtca cagagctaac teegtgtgag acagagaate ceatgggagg 360
atatggcaaa accattagcc atgtgatcat aggactcaaa acagccaaag gaaccaaaca 420
gttgaaactg gaccccagca tttttgaaag tttgcagaaa gagcgagtag aagctggaga 480
tgtgatttac attgaagcca acagtggggc cgtgaagagg cagggcaggt gtgataccta 540
tgccacagaa ttcgaccttg aagctgaaga gtatgtcccc ttgccaaaag gggatgtgca 600
caaaaagaaa gaaatcatcc aagatgtgac cttgcatgac ttggatgtgg ctaatgcgcg 660
gccccagggg ggacaagata tcctgtccat gatgggccag ctaatgaagc caaagaagac 720
agaaatcaca gacaaacttc gaggggagat taataaggtg gtgaacaagt acatcgacca 780
gggcattgct gagctggtcc cgggtgtgct gtttgttgat gaggtccaca tgctggacat 840
tgagtgcttc acctacctgc accgcgccct ggagtcttct atcgctccca tcgtcatctt 900
tgcatccaac cgaggcaact gtgtcatcag aggcactgag gacatcacat cccctcacgg 960
catccctctt gaccttctgg accgagtgat gataatccgg accatgctgt atactccaca1020
ggaaatgaaa cagatcatta aaatccgtgc ccagacggaa ggaatcaaca tcagtgagga1080
ggcactgaac cacctggggg agattggcac caagaccaca ctgaggtact cagtgcagct1140
gctgaccccg gccaacttgc ttgctaaaat caacgggaag gacagcattg agaaagagca1200
tgtcgaagag atcagtgaac ttttctatga tgccaagtcc tccgccaaaa tcctgggctt1260
gaccaggcag ggataagtta cattgaagtt gagatggctt gagggttttt cagcagctaal320
gagacttccc caggtgtgcc tggcctgggg tccagcctgt gggcgctttg ccctggggtt1380
tgggggctgc ccttccccat tcaggcgttg ggttgcagcg ttgttcaatt tcagttgttg1440
gaaagcgttt tttttttgaa gttagtctta agtgtttccc cttgggtttg ttttgaaaag1500
aacccttcct
                                                                 1510
```

(2) INFORMATION ON SEQ ID NO. 59:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1188 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```
gagaactcac accatatgtg teetgtteea gtgegegggt etgtggagag eegggtgega
geggeggeag cacgaggga aaagagetga geggagaeca aagteageeg ggagaeagtg 120
ggtctgtgag agaccgaata gaggggctgg ggccacgagc gccattgaca agcaatgggg 180
aagaaacaga aaaacaagag cgaagacagc accaaggatg acattgatct tgatgccttg 240
qctqcaqaaa taqaaqqaqc tqqtqctqcc aaaqaacaqq aqcctcaaaa qtcaaaaqqq 300
aaaaagaaaa aagagaaaaa aaagcaggac tttgatgaag atgatatcct gaaagaactg 360
qaaqaattqt ctttggaagc tcaaggcatc aaagctgaca gagaaactgt tgcagtgaag 420
ccaacaqaaa acaatgaaga ggaattcacc tcaaaagata aaaaaaagaa aggacagaag 480
qqcaaaaaac aqaqttttga tgataatgat agcgaagaat tggaagataa agattcaaaa 540
tcaaaaaaga ctgcaaaacc gaaagtggaa atgtactctg ggagtttaac aaacttccta 600
aaaaagctaa agggaaagct caaaaatcaa ataagaagtg ggatgggtca gaggaggatg 660
aggataacag taaaaaaatt aaagagcgtt caagaataaa ttcttctggt gaaagtggtg 720
atgaatcaga tgaatttttg caatctagaa aaggacagaa aaaaaatcag aaaaacaagc 780
caggitectaa catagaaagi gggaatgaag atgatgaege eteetteaaa attaagaeag 840
tggcccaaaa gaaggcagaa aagaaggagc gcgagagaaa aaagcgagat gaagaaaaag 900
cgaaactgcg gaagctgaaa gaaaaagaag agttagaaac aggtaaaaag gatcagagta 960
aacaaaagga atctcaaagg aaatttgaag aagaaactgt aaaatccaaa gtgactgttg1020
atactggagt aatteetgee tetgaagaga aageagagae teecacaget geagaagatg1080
acaatgaagg agacaaaaag aacgaaagat aagaagaaaa agaaaggagg acaagggagg1140
aaaaqaqaac aqaqaaqqaa aqaaqqqcct qqcaaaaqcc actqtttc
```

(2) INFORMATION ON SEQ ID NO. 60:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2208 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

				*		
gcaggacggc	tctgggccct	tcctggctga	cttcaacggc	ttctcccacc	tggagctgag	60
				gcgctggagg		
ggcacgaggc	cccagcggcc	tcctgctcta	caacgggcag	aagacggacg	gcaaggggga	180
cttcgtgtcg	ctggcactgc	gggaccgccg	cctggagttc	cgctacgacc	tgggcaaggg	240
ggcagcggtc	atcaggagca	gggagccagt	caccctggga	gcctggacca	gggtctcact	300
ggagcgaaac	ggccgcaagg	gtgccctgcg	tgtgggcgac	ggcccccgtg	tgttggggga	360
gtccccggtt	ccgcacaccg	tcctcaacct	gaaggagccg	ctctacgtag	ggggcgctcc	420
cgacttcagc	aagctggccc	gtgctgctgc	cgtgtcctct	ggcttcgacg	gtgccatcca	480
gctggtctcc	ctcggaggcc	gccagctgct	gaccccggag	cacgtgctgc	ggcaggtgga	540
cgtcacgtcc	tttgcaggtc	acccctgcac	ccgggcctca	ggccacccct	gcctcaatgg	600
ggcctcctgc	gtcccgaggg	aggctgccta	tgtgtgcctg	tgtcccgggg	gattctcagg	660
accgcactgc	gagaaggggc	tggtggagaa	gtcagcgggg	gacgtggata	ccttggcctt	720
				gagagcgaga		
gagcaaccac	tttgaactga	gcctgcgcac	tgaggccacg	caggggctgg	tgctctggag	840
tggcaaggcc	acggagcggg	cagactatgt	ggcactggcc	attgtggacg	ggcacctgca	900
actgagctac	aacctgggct	cccagcccgt	ggtgctgcgt	tccaccgtgc	ccgtcaacac	960
caaccgctgg	ttgcgggtcg	tggcacatag	ggagcagagg	gaaggttccc	tgcaggtggg1	1020
caatgaggcc	cctgtgaccg	gctcctcccc	gctgggcgcc	acgcagctgg	acactgatgg1	080
				ccagcactgc		
cggcacaggc	tttgtgggct	gcttgcggga	tgtggtggtg	ggccggcacc	cgctgcacct1	1200
gctggaggac	gccgtcacca	agccagagct	geggeeetge	cccaccccat	gagctggcac1	L260
cagagccccg	cgcccgctgt	aattattttc	tatttttgta	aacttgtcgc	tttttgatat1	L320
gattttcttg	cctgagtgtt	ggccggaggg	actgctggcc	cggcctccct	tccgtccagg1	1380
cagccgtgct	gcagacagac	ctagtgctga	gggatggaca	ggcgaggtgg	cagcgtggag1	1440
ggctcggcgt	ggatggcagc	ctcaggacac	acacccctgc	ctcaaggtgc	tgagcccccg1	L500-
ccttgcactg	cgcctgcccc	acggtgtccc	cgccgggaag	cagccccggc	tcctgaatca1	L560
				ggggctgctg		
gggcccttcc	tccgggtgac	cccacagggc	ctttccaagc	ccctatttga	gctgctcctt1	L680
cctgtgtgtg	.ctctggaccc	tgcctcggcc	tcctgcgcca	atactgtgac	ttccaaacaal	L740
tgttactgct	gggcacagct	ctgcgttgct	cccgtgctgc	ctgcgccagc	ccaggctgct1	1800
gaggagcaga	ggccagacca	gggccgatct	gggtgtcctg	accctcagct	ggccctgccc1	1860
agccaccctg	gacatgaccg	tatccctctg	ccacacccca	ggccctgcga	ggggctatcgl	L920
				gcctgggtat		
ccatggctgt	gttcttcatg	tgttgatttt	atttgacccc	tggagtggtg	ggtctcatct2	2040
				caaaatcctc		
				aaggggccaa		
			aggttggaag			2208

- (2) INFORMATION ON SEQ ID NO. 61:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 283 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

gaaaaggggg agggggagtg acaatctttg cttggggcct atgacttctc cagccccaag 60 gggagatgcc accgggaaat cccccaatgt ccactagggg gcaggaggcc accgttcttc120 gtactccgga gaacctggct ggagagctct ttcttgttca cccttccctc cagctgtatc180 tctgccctgc agataacgtg aaggactgga gcaaggtcgt cctggcctat gagcctgtgt240 gggccattgg tactggcaag actgcaacac cccaacaggg aac 283

- (2) INFORMATION ON SEQ ID NO. 62:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 184 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

aacggaggat gcctaggctt ctggaggcga agaaggacgc ggcaagctgc gaaaagtcac 60 gggtatctgc aagcatgaaa tgatccgtga atatccgaat ggggcaaccc gtgcaggtga120 agcctgcaca cctgaataaa tcaggggcag acgcagggaa ctgaaacatc ttagtacctg180 cagg

- (2) INFORMATION ON SEQ ID NO. 63:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1780 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

tecceeceg gggcaacece eccateggge ecceaaageg etggggttac ageettaage 60 caccaaqccc cggccgacct tcttctattt ttccattctc ctttccaaag ccatqqccat 120 qcqctcctqt gtacaggtqc ataaacacat cagtqtqcca tccctcacat gcatqtcqtt 180 coccaccet cetteccagg gettetettg getecagegt teetetggga ceetetgeag 240 atacageetg tgetggacce ceagecaggg tgagggetea ttetgetetg tetteceeae 300 tgcctcagtt tcccccaaaa gctgctttca cgtccttcta gtagggggcc tcccatgggg 360 qcaaqqatcc cctttaggat tcaatctttc ctctttgggc agttttggct ttgaqtcccc 420 cagggatcag ggtgagaatg aagaagagct cagtgagcgg aatgacagca gctgggtggg 480 tqqtqtqqqq agaggctgag gggaaggcag ctctaagact gggagtggag ttcctggagg 540 tqtqqqqqq qqqqcqtqtt ttcaatttag aaaaatctca gccagctcga gccqaqaqag 600 aatgcgaaag aggaagttcg gaaggagcga ggaatggggt gggtggcagc gggggccgct 660 caqttqctgt cgctcttgtc caccagcacg gcgtccgact cctcggtgat ctccagcagc 720 gegtgeaegt eggggetget eeeggeege aggtegeegg eetceeeeg eteegeeeae 780 ctccaccatc teggtggect tgagcactte cacctggece tegeggatet tettgaegtg 840 gaaggtgaag ggtggcacct tgtagaccgc ggtcttggag cgcgcgtaca ccacgtggtc 900 gggcgtgaag gatttgcgca acttgtcccg cgacgtcttc agtttctcgc gccgctcggc 960 gggcaccagg cgcgtgccca gcttgttcat gcgcttctcc agggtgtgcc gcgtcttctc1020 caggttttcc ttggtcttga ggcgcgtctt ctccaggttc tcgcgggtac gcaccttggt1080 cttctccatc ttctccttgg agaaggcctt cttgaagtcg tccacgcgcc gcaggccctg1140 cgcttgatac gctctgcgcg ggactcctca ataacctcct caacctccac cgcctcgtcc1200 gacgaaaget ccagegeege tgcgteetee tegggeeget egecetegee eageteeteg1260 content of the conten ggcagettea etteateetg gtagateatg aetttaaagt tgeggegeeg cageageteg1380 geotegttga cotecagett ettgatetge ecegeetgge getecagget geogegeaeg1440 gtetteacgt tgacgetgac ettgegeace ttetecagea gettgeteac egtattgete1500 qtqqtqqcqt qcqccttqcc caqcttqctc agctcqccct ggatqctctq cactqcqccc1560 tocatotocq cotqcoqctc ctccagetqt gottqaqtca gotqqatotq gtctacqqcc1620 ccgatgattt tgtccaggag gctcagcacc agcacgccgt tcacctggtc cgacttgatc1680 agetettetg ageeggeece egaeggetee teegetgeet gageeceage ggaggaaget1740 ccqqqqcctc qqcqatcqqq qtacccqqqc aaqcqqccqc

(2) INFORMATION ON SEQ ID NO. 64:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1652 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```
ctcgagcggc tcgagccgat tcggctcgag cggctcgaga agaagatatg ctagtctgta
tttttgctgt gctattgagg atcaggacaa tgaactaatt accctggaaa taattcatcg 120
ttatgtggaa ttacttgaca agtatttcgg cagtgtctgt gaactagata tcatctttaa 180
ttttgagaag gcttatttta ttttggatga gtttcttttg ggaggggaag ttcaggaaac 240
atccaagaaa aatgtcctta aagcaattga gcaggctgat ctactgcagg aggaagctga 300
aaccccacgt agtggttctt gaagaaattg gactgacata actctcctcc cttgttgatg 360
acttettgtg geattteaca cactgtagat ggteactece tteatgteea tgttagetea 420
tggtgtaaga tgatgtcttg tcagtattac tgttttgcta agccgcttca ttcatgccta 480
cacaattttt ttttaaaagg gaactttagt taattaagtg ataagggact taaatatgaa 540
ttagaatggt gcagaaagag ataccttttc tggatatttt aaagtttaaa ggtcagtttc 600
tottaatotg attatgtgca catatgaaaa tggcacatca tatacatgta aaatcaggca 660
gtatacattt attaattact gtatttgaca aaggaaactc ttaaattata atgtgaaacc 720
tggttttatg aaaccaaaga ctagtgcagc atttcagcat atgtaaaaag aaaaaaaaa 780
gggaattgac atgtcacata tcaaatgaat ggaaactttg ttgaaacttt aaaaagcaaa 840
tttactccaa agacttgtat tggaaattac ataccttttt ttttttttt aaaggactac 900
agattatttt taatgactaa attggagtga tacttcttac actaaaaatt atttcttagg 960
cattetgaat etgggatgag aaacaggatt gtttcacaat agtaagcaca taatttttaa1020
ggccaaggca catttgactc ctgagatgaa ttttttgtgg tcataatcaa atacttagtt1080
gtttttgatg ccccaaaata aagtgagaat ggtaatttgc caggaattct tcataacagt1140
atcttacaaa aaacgtgttg ctctcttcac agtattatgt gtaaagtcat tgtttaaagc1200
acgaatgttc cctctggggt acttgttaaa gctaaattta ttttgcttcc ctccacttag1260
aagtgctgca cactttacag cagcttcctt tctttccatg gcactgccta gttaacagaa1320
gtcttataaa aatttaaaaa gacacatttc ttacaaaaaa gagttgaatg aggtaaaatg1380
gcattagatg gctctatatt ttttaaagct atgtaattgt tcagcgtcac ttttctaagt1440
acttatacat atctaaacat gtcttcatgg tttatatttt cacttatata tgctgggctg1500
gattaagett tgttgtgatt gtgaccaaca ttcaggccac gtgagcactg tettatcaca1560
togocaatta gttgtaataa acgttcaacg tacaaaaaaa aaaaagggcg cagcttccct1620
ggggggaatt actggaagcg gggttaagcg ga
```

- (2) INFORMATION ON SEQ ID NO. 65:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1085 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```
getecetgge etecetetea gacagettgg gggtgtetgt catggecace gaccaggact 60
cctactccac cagcagcacg gaggaggagc tggagcagtt cagcagcccc agcqtgaaqa 120
agaagccctc catgatcctg ggcaaggctc ggcaccggct gagctttgcc agtttcagca 180
gcatgttcca cgctttcctc tccaacaacc gcaagctgta caagaaggtg gtggagctgg 240
cgcaggacaa gggctcgtac tttggcagcc tggtgcagga ctacaaggtg tacagcctgg 300
agatgatggc gegecagace tecageaegg agatgetgea ggagattege accatgatga 360
cccagctcaa gagctacctg ctgcagagca ccgagctcaa ggccctggtg gaccccgccc 420
tgcactccga ggaggagctc gaagcaattg tagagtctgc cttgtacaaa tgtgtcctga 480
agcccctgaa ggaagccatc aactcatgcc tgcatcagat ccacagcaag gatggttcgc 540
tgcagcagct caaggagaac cagttagtga tcctggccac caccaccact gacctaggtg 600
tgaccaccag cgtgccggag gtgcccatga tggagaagat cctgcagaag ttcaccagca 660
tgcacaaggc ctactcacct gagaagaaga tctccatcct gctcaagacc tgcaaactca 720
totacgacto catggocoto ggcaaccoag ggaagcocta tggggcggat gacttoctgc 780
ctgtgctcat gtatgtgctg gcccgcagca acctcacgga gatgcttctc aatgtggagt 840
acatgatgga gctcatggac cccgccctgc agctggggga gggttcctac tatctgacca 900
ccacctacgg ggccctggag cacatcaaga gctacgacaa gatcacggtg acccggcagc 960
tgagtgtgga ggtgcaggac tccatccacc gctgggagcg ccggcgtact ctcaacaagg1020
cccgggcctc ccgctcctcc gtacagccac ttcatctgcg tgtcgtacct ggagcccgag1080
cagca
```

- (2) INFORMATION ON SEQ ID NO. 66:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1393 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

gggcagggga gggagttgac gggctgacac aggaaactcc cctgaaacct gtttctcagc 60 ttcccggccc agctggggca cccactggaa ggagaggcca ggcggaagac cctggctccg 120 teatggcete tgccctgagg ccaccccgtg tccccaagce taagggtgte ctgccttcac 180 actactatga gagctttcta gagaagaagg ggccctgtga ccgggattac aagaagttct 240 gggcaggcct gcagggtctc accatttatt tctacaatag caatcgggac ttccagcacg 300 tggagaaget caacttggga geatttgaga aacteacaga tgagatteee tggggaaget 360 cacgtgaccc tggcacccac ttcagcctga ttctccggaa tcaggagatc aagttcaagg 420 tagagacctt ggagtgtcgg gaaatgtgga aaggcttcat cttaacggtg gtggagctcc 480 gtqtcccgac cgacttgacc ctgcttcctg ggcacctata catgatgtct gaagtcttgg 540 ccaaagagga ggcgccgt gcactggaga caccctcgtg cttcctgaag gtgagccggc 600 tggaggcaca actgctcctg gagcgctacc ccgagtgcgg gaacctgctg ctgcggccca 660 geggggaegg egeegaeggt gteggteace acgeggeaga tgeacaaegg gaegeaegtg 720 gtccggcatt acaaggtgaa gcgggagggg ccccaagtac gtgatcgatg tggaacagcc 780 gttctcttgc acctccctgg acgccgtggt caactatttc gtgtcgcata ccaaaaaggc 840 gctggtgcca ttcctgttag acgaggacta cgagaaggtg ctaggctacg tggaagccga 900 taaggagaat ggcgagaatg tgtgggtggc gccctccgct ccgggcccag gtcctgcacc 960 ctgcacaggt ggccccaagc cgctgtcacc tgcgtctagc caggacaagc tgccccact1020 gcccccacta ccgaaccagg aagagaacta cgtgacccct attggagatg gcccagctgt1080 tgactatgag aaccaagatg tggcttcctc tagttggcca gtcatcctga agccaaaqaa1140 gttgccaaag cctcctgcca agcttccaaa gccacccgtt ggacccaagc cagagcccaa1200 agtetttaat ggtggettgg geagggaage tgeeagttea gttteageee ageetettet1260 ttccccacag gccgggctgg gcagacatgg acggcagagt tacagaagaa gctgggagaa1320 gaggcggggc actggtagca tggtttcgga cacaccaggg accagcgggt tagttccagg1380 gcgggccagg tgg 1393

(2) INFORMATION ON SEQ ID NO. 67:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1248 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:
qqcacqaqqa aqttaaqatc atacatqcqq atqtqctqqt aacctqcaaq aaqcaatcat 60
gctgcggtcc ggtgtgacct cccaaggcat tcaccctggg agtccctggt gctgcacccc 120
aacccaggca gagctcatcg tgggtgacca gagcggggct atccacatct gggacttgaa 180
aacagaccac aacgagcagc tgatccctga gcccgaggtc tccatcacgt ccgcccacat 240
cgatcccgac gccagctaca tggcagctgt caatagcacc ggaaactgct atgtctggaa 300
tetgacgggg ggcattggtg acgaggtgae ccageteate eccaagaeta agateeetge 360
ccacacgcgc tacgccctgc agtgtcgctt cagccccgac tccacgctcc tcgccacctg 420
ctcggctgat cagacgtgca agatctggag gacgtccaac ttctccctga tgacggagct 480
gagcatcaag ageggeaace eeggggagte eteeegegge tggatgtggg getgegeett 540
ctcgggggac tcccagtaca tcgtcactgc ttcctcggac aacctggccc ggctctggtg 600
tgtggagact ggagagatca agagagagta tggcggccac cagaaggctg ttgtctgcct 660
ggccttcaat gacagtgtgc tgggctagcc tgtgacccct cgggactgcc tggtgcaggt 720
ggtggcaget ggagggacce atgcagcace caggtcagag cagaccetee cetgeeggee 780
tgcgccactg gacctgatgg ccccctgtgg cgccttgacc tgctgggcca ggctgccctg 840
ggacteteag ecceeagttg ettateeaga tgtgaeagag etegaeeeaa geeaggetge 900
acactectgg actgggetag cetgeactge etgggaaagt eggeegaggg eccaaagetg 960
ctgaggggtc tgaggctggt gcccaccccc aagctagtgt gttctctgcc cctccctgcc1020
cgcgtttcag ggcctcggtc catagagaac accaccacca tggccaggtg gaagggttta1080
ttagtccctg ccagcagctg tcctccctgg tgcaggtggc ctggccagcc cactggattg1140
gggacgggcc aggctgggcc aggtcggggg ctcagtctgg gaggtaataa aagcagaccg1200
acacgcagat gttgctcggg aaaaaaaaaa aaaaaaaaa aaaaaaaa
                                                                 1248
```

- (2) INFORMATION ON SEQ ID NO. 68:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1099 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

ctcgtgcaat ttcgggcagg gagtgtcaag cctgttgtct taacattttg tataaaaaag 60 aacaacagaa attatctgtc atttgagaag tggcttgaca atcatttgag ctttgaaagc 120 agtcactgtg gtgtaatatg aatgctgtcc tagtggtcat agtaccaagg gcacgtgtct 180 ccccttggta taactgattt cctttttagt cctctactgc taaataagtt aattttgcat 240 tttgcagaaa gaaacattga ttgctaaatc tttttgctgc tgtgttttgg tgttttcatg 300 tttacttgtt ttatattgat ctgttttaag tatgagaggc ttatagtgcc ctccattgta 360 aatccatagt catctttta agcttattgt gtttaagaaa gtagctatgt gttaaacaga 420 ggtgatggca gcccttccct agcacactgg tggaagagac cccttaagaa cctgacccca 480 gtgaatgaag ctgatgcaca gggagcacca aaggaccttc gttaagtgat aattgtcctg 540geeteteage catgacegtt atgaggaaat atcccccatt egaacttaac agatgeetee 600 tctccaaaga gaattaaaat cgtagcttgt acagatcaag agaatatact gggcagaatg 660 aagtatgttt gtttattttt ctttaaaaat aaaggatttt ggaactctgg agagtaagaa 720 tatagtatag agtttgcctc aacacatgtg agggccaaat aacctgctag ctaggcagta 780 ataaactctg ttacagaaga gaaaaagggc cgggcacagt ggcttattcc tgtaatccca 840 acactgtqqa aqqccqaqqc aqqaqqatca cttqaqtcca qqaqtttqaa acctacctaq 900 gcaacatggt gaaaccttgt ctctaccaaa ataaaaatta gctgggcatg gtggcacgtg 960 cctqtqqtcc caqctacttq qgaqqctqaq qtqqqaqcct qqqaqqtcaa qqctqcaqtq1020 agccatgate atgccactge actecateet gggtgacage aagatettgt etcaaaaaaa1080 aaaaaaaaa aagtcgacc

(2) INFORMATION ON SEQ ID NO. 69:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 774 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

- (2) INFORMATION ON SEQ ID NO. 70:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

tagctccagt ctcagctgta tcatttcta actgatttt acaataaaaa tgagagtaaa 60 aatcagttac tctttctaga cattaattag cacatttacg ttaagactct aagtagtata120 aaatgtaaat tgctgctacc ctactaagtt actgtcagta aatactgtgt gcagtaaatg180 ttgagtatgg attaattgaa ggatacctct acaattattt cctttagtca aggttgtagc240 taagaattgg gcttctgaca tacattcttt ttaatctttt tcgtattggg ttttatagca300 ctaaacctaa tttctaacat attttacac ctgaaatcta cattctaata taaaggtttt360 tttttataac gttcctaaaa tttcaggccc tcagcaggca gtttttgtcc cagttttctt420 caacag

(2) INFORMATION ON SEQ ID NO. 71:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1417 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```
gccaacette ectececcaa ecetggggee geeceagggt teetgegeae tgeetgttee
tectgggtgt cactggeage cetgteette etagagggae tggaacetaa tteteetgag 120
gctgagggag ggtggagggt ctcaaggcaa cgctggcccc acgacggagt gccaggagca 180
ctaacagtac ccttagcttg ctttcctcct ccctcctttt tattttcaag ttccttttta 240
tttctccttg cgtaacaacc ttcttccctt ctgcaccact gcccgtaccc ttacccgccc 300
cgccacctcc ttgctacccc actcttgaaa ccacagctgt tggcagggtc cccagctcat 360
gccagcctca tctcctttct tgctagcccc caaagggcct ccaggcaaca tggggggccc 420
agtcagagag ccggcactct cagttgccct ctggttgagt tggggggcag ctctgggggc 480
egtggettgt gecatggete tgetgaeeea acaaacagag etgeagagee teaggagaga 540°
ggtgagccgg ctgcagggga caggaggccc ctcccagaat ggggaagggt atccctggca 600
gagteteeeg gageagagtt eegatgeeet ggaageetgg gagagtgggg agagateeeg 660
qaaaaqqaga gcagtgctca cccaaaaaca gaagaatgac tccgatgtga cagaggtgat 720
gtggcaacca gctcttaggc gtgggagagg cctacaggcc caaggatatg gtgtccgaat 780
ccaggatgct ggagtttatc tgctgtatag ccaggtcctg tttcaagacg tgactttcac 840
catgggtcag gtggtgtctc gagaaggcca aggaaggcag gagactctat tccgatgtat 900
aagaagtatg ccctcccacc cggaccgggc ctacaacagc tgctatagcg caggtgtctt 960
ccatttacac caaggggata ttctgagtgt cataattccc cgggcaaggg cgaaacttaa1020
cctctctcca catggaacct tcctggggtt tgtgaaactg tgattgtgtt ataaaaagtg1080
gctcccagct tggaagacca gggtgggtac atactggaga cagccaagag ctgagtatat1140
aaaggagagg gaatgtgcag gaacagagge gtetteetgg gtttggetee eegtteetea1200
cttttccctt ttcattccca ccccctagac tttgatttta cggatatctt gcttctgttc1260
cccatqqaqc tccqaattct tgcgtgtgtg tagatgaggg gcgggggacg ggcgccaggc1320
attgttcaga cctggtcggg gcccactgga agcatccaga acagcaccac catctaacgg1380
ccgctcgagg gaagcacccg gcggtttggg cgaagtc
                                                                 1417
```

(2) INFORMATION ON SEQ ID NO. 72:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 691 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

(2) INFORMATION ON SEQ ID NO. 73:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1705 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```
gattcggcat gaggacagag ccctttttga aaataaattg gcattggagt gttttaccct
ctagctgttt tacttagaat gtaacatatg ctgcctaccc acctcaaaat gtctgtactg 120
caagagggcc ctgggcctct gctttccata ttcacgtttg gccagagttg tagtcccaaa 180
gaagagcatg ggtggcagat ggtagggaat tgaactggcc tgtgcaatgg gcatggagca 240
caaggggtca cagcatgcct cctgccttac cgtggcagta cggagacagt ccagaacatg 300
gtcttcttgc cacggggtgt tgttgtctct ggtggtgctg catgtctgtg gctcaccttt 360
attettgaaa etgaggttta eetggatetg getaetgagg etagagecea eageagaatg 420
gggttgggcc tgtggccccc caaactaggg ggtgtgggtt catcacagtg ttgccttttg 480
tetectaaag atagggatet aettttgaag ggaattgtte eteccaaata aatttgettt 540:
accttggtcc tttcttttgt gccagtattc aagtggtata gctctgagca gggtcacatt 600
tggccaaacc tgacactgtc ttgctgcatt ctcctttggc aaacatcagg gtcagaattc 660
aggatagece tteetaggge actggaettt etggeatggg ggetgtgttt geacaagtta 720
ttttcatgtt acctggagag tgtccagagg ctgctctgag gctgaggtgt gttccccctt 780
gcctggttcc agctgtcaga gggataccat cctagggtct gggaatccaa ggccacgaga 840
ctccttggtt tgtggtccga gatcctgtac taaggagggt ctggccagag gaacagacca 900
gettttgeae aatgaagege aagggaaeaa gtggtttgee tggtgteeta eetgteetga 960
acctggtcct gtgggccatt gaaaagttag atctgtgatc tctggggttt ttgtggcttt1020
gttcaatget tecaetetag ggeaggeaga geagtetata eteteceaag eetgettgae1080
ctccaagtag agctgataca gagatctgtg aatattgtga tagaaattct ttggtattcall40
tacatttcag ctgcaagtca gcaatttccc aggtaccatg taagctataa aacagtcatt1200
cttaaagaca gaggatagct gtgactcatg ggatcatgag gtccatggct ggttgcaggt1260
tecettttte etteeteagg ttttgtetet teetgtgttg teeceageaa gggagagaet1320
gtggggtgga ttgggagaac agattaggag tatagcaaat gaacccagaa tggaacagtg1380
gggagctaac tgtgaatgag gagagtacct gctgcaggac ctggaggtca ggtgtgaatg1440
ctgtattggc acagggaata aatatcctgg cgtctggagc cttcacctct ccgtcaagtc1500
cttcctgtga tactgccatg gcacaggatc tgagttgcag ctctgcaccc taaatcacac1560
cctgggcatt gtctgggctg cagggctgcc aggttctgta cttgtgtcca gctgtggccc1620
tggatgccgg aaactgggag gggtttcttg tgcccagaat gtagcctgta acgcttgggc1680
gccttttaaa gcccccctg gggcc
                                                                  1705
```

(2) INFORMATION ON SEQ ID NO. 74:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1516 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

gtttattctt agtagttgga actaatgtag tctgactaaa atacacatgg gtgtctgctc 60 tgtgatgttt aaacttatct gttttgtttg gttttcattt caggaagcag aagtgcaagc 120 aaagcagcaa gcatgaacct taagcactgt gctttaagca tcctgaaaaa tgagtctcca 180 ttgcttttat aaaatagcag aattagcttt gcttcaaaag aaataggctt aatgttgaaa 240 taatagatta gttgggtttt cacatgcaaa cattcaaaat gaatacaaaa ttaaaatttg 300 aacattatgg tgattatggt gaggagaatg ggatattaac ataaaattat attaataagt 360 agatatcgta gaaatagtgt tgttacctgc caagccatcc tgtatacacc aatgatttta 420 caaagaaaac accetteeet eettetgeea ttactatgge aacttaagtg tatetgeage 480 tctacattaa aaaggagaaa gagaaataac ctgtctctca ttcctaagtt gcctcattaa 540 ttttcatgaa caagaatatg tacctttttg atgctatatt actgcgatta aaaagttctt 600 gcaggtaatg tttatgatat gttaaacgtt gtaatttctt atcgtaatta taacattccc 660 attettttgt agatgaaact tetacatatt gaaccacaga ttttetgage ttetaaatgt 720 agcettteat tgcacattte agtgateaga atagatatee ttttacaege acaaaageaa 780 tagattcatt cagtggacaa gttccttgtt taactacaca gctatgatgg aatgatatat 840 ccaagtteet tgeeteagtg aaatatgeat atgtatatea tgaaagtggg atgeeaagta 900 agettaaaat ggeattetet ageaaagaga ttagaetttt aaataaetet tataaaacag 960 gttggcgatc atttcccaag attggtttcc cttgagtttt tgctaaaaca aatcttagta1020 gttttgcccg tttaaaacaa ctcacaatcg taaatgctac tattcctaag atatcttacc1080 tttttatttc agtttagcca tgtattgtat gagtgtatta gtctaagcag tgagaatctt1140 ttctatgcct ctattccagc aaaaagtaga agtatcaaat aaaaagggca acttttaaaa1200 tattaagcct gaagacttct aaaaagacaa gaaacatggc ctaaataacc aacatagatt1260 tacatagtaa gtttcacact accttattac caaaagcaaa cacctcttac tttaaactac1320 attatcatgt atatctattg tatgctggtc tttacttttt gccaaaatca acatataatg1380 aagagatgcc tttgtttcat gagattcaaa cttgatgcta tgctttaaaa taaactcagt1440 acttttagaa acataaaaaa aaaaaaaaa aggcgacccc ccgagtagtg ggcccgcgcc1500 cggggatttt tccggg

(2) INFORMATION ON SEQ ID NO. 75:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1490 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

gaataaaggg ctggccagac ccagtggcgt cctttcccag acctttcttg gcacaaagcc 60 tttgctgcct ggcttggagg ccctgcggcc tacattctct ggaccccact atgtgcctgg 120 caaagggcta gtgccttgag gaaactgagg tagctgggtt ggtccccttc caggaattca 180 qaqtctqqtq qcaggggcat gggaaataga cagatgtaat tctatagcct gggcctggca 240 coetceacet ccaegeecea ccageattge ettaegeete cettgeecea egttagatgg 300 tttcttccgg ttttgcactc tggctgcccc ttggagtctc ctggggagct gtaatatctc 360 tttggagatt cagattgagc tggtctaggt tgtggcccag gcattgggca ttttggaagc 420 ccccaggtgt tttcagcttg cagccaggcc gagagagagc ccctgagtca gatccccatg 480 gtttaggcac acctageggg aggggtggct cetggacece accgtggttg gagagetgag 540 catgtgtgtg gctttagtgg ggtctgttag ttatgggggt ctgggcactg gagctgcagg 600 acacttggga tcccaggtca gaaagggcca gatgagcaac taggaaagac ttgggggcca 660 gggcggagtg gggtcacctg acactettgt gaggcccctt ctagtgcctg ctcacaccgg 720 aatttcattc actccaagaa gccatcaggg gtaagatacc ttcctttaaa cgtcactaag 780 aaagaagagg cctgccggtg acacagtaag atgccattga tctaaagatg cgtcttgatt 840 tcaqaaaqqt ccqqaaqtqq aaaqcaqqtt tcaqqqctqc tqaqqtacaq gqttctcctq 900 taggccccag ggatggtctc aggggtgctg agtgcgtgcg tggtaaatgg atggagccca 960 ggggcgcctc ctgccagtgt cctccaggca ctcaaaccta gcccttctga agccgacctc1020 acgtgacete acageceete etgaaggege etcactgatg acggtgggtg gaataacage1080 ccccagagat gtccaggttt ggaaccccag gacgtgggaa agtgttacct tgcgtggcaal140 aagggacccg gcgcctgtgc ttcagttcag gatttcgtgg tggggagatg accgtggatg1200 gttgaggtgg gccctgagta atcatggggg cccttataag ggaaggggag tcacgagggt1260 ctgcgcatga agcaaggaag cttctggctg tgaagatggc aagaaggcct ggggccaggc1320 gatgaggtgg cccctggagg agctggaaaa ggcattggat tctgccccag agcctccgtg1380 gagaaacaaa gccgcactga caagacttca gcctggtgaa aaccattttg gactcctgac1440 ctctagaact gtaagataat aaattggtgt ggttttcaac ctctcaaatg 1490

(2) INFORMATION ON SEQ ID NO. 76:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2513 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

ctcgagccga ttcggtttca gcagaaagtg atggaaaaag aaactgaaaa gcgcatttct gaaatcgaag atgctgcatt cctggcccga gagaaagcga aacaagatgc tgaatattat 120 gctgcacaca aatatgccac ctcaaacaag cacaagttga ccccggaata tctggagctc 180 aaaaagtacc aggccattgc ttctaacagt aagatctatt ttggcagcaa catccctaac 240 atgttcgtgg actcctcatg tgctttgaaa tattcagata ttaggactgg aagagaaagc 300 tcactcccct ctaaggaggc tcttgaaccc tctggagaga acgtcatcca aaacaaagag 360 agcacaggtt gatgcaagag gtggaaatgt tctccatatc aagatgtggc ccaaggggtt 420 aagtgggaac aatcattata cggactette agatttacag agaacttaca etteatetgt 480 tccacctctc ctgcgatagt cctgggtgct ccactgattg gaggatagag ccagctgtct 540 gacacacaaa tggtcttttc agccacagtc ttatcaagta tcctatatgt attcctttct 600 aaactgctac tcatgaatga ggaaagtctg atgctaagat actgcctgca ctggaatgtt 660 aaacactaaa tatataacaa gctgtgtttt cctaagctga gatctgttga ataatgttta 720 cattegteec eeggggaaat gtatgeteag ceaceattea agagatgaet gagaaggaga 780 tggtaagttc aagaagactg attgcacctg ggacccaggc cctttctttg ggatccagtc 840 ccagcettca tecatgtgat taagatecag geogetgaag tteeccagga aatgatette 900 cacttgagca accttttact tgatacgatt tgcacctttc tgttttcctg cagtcagggt 960 ggtggcctgc agggacctga gctttgctac ccaaccagat tcctcataga gattcctaat1020 cactagtttc ttgtattcat aaactcagag atacagaggg cttggtttga agttggggtg1080 agatgaaacc tttgctctga gccaaagctc tggggccttg cattccctgc attgggttgal140 tgactgtcag catcactgcc gcagcatgct tgactaaggt acctggtttt agccacagcc1200 acctccttgt.atgttacctt tcagctctgg ccaagagtgg gacagggttt taaccacaaa1260 taggagcagc atgcaattcc tagtgacttg ctgcacagta ttgtatcata attacaggaa1320 gtttttattt ttaaaactgg atctggggta tattcatttg ccccatcacc tctgtctaaa1380 ggcccaagtc ctagggctgc catggtcaca agcacactga tgctccttaa gattgtttat1440 ctggagccca catagtgtgg aacaaaaagt cacctagaaa gcatccttgg tcatcattgt1500 ctccttccca cctggcccag agatgcttaa atccaagttg tttctccagc tgtcacctcc1560 cccaggagat caggattcca ctgacgtcct gggcagccag tgaatttaat tttccatgag1620 aaacaacaga gttaacctgt ggcattagga gacctacttc atgtggaccc tttttttcct1680 tcagtttaac ttttctggag cagtgtgctg cgtagttcgg cctgagtttg tgcagcttgt1740 taagacaact cttgtgtacg ctatgttgaa gctcaacaaa aaagtcatgg gaccacttct1800 agaaatcttt cagctgtcag gcctgtcagt ctcatgacag tttgttggtt gtgccaaaca1860 ctttatttgg gaaaggaaag cccagatttg aatgggtctt tcccctgggc cttatcctat1920 agaggcattt gtaatatgga gaaaataatt tttcattttt gctcatttaa ttctataaat1980 tctctttata aatgaatttt gtgttcttta gttctcctta aaagaacttt tgaattataa2040 aaataaaatc tttacctgtc gaattgttgc tgcagatgat tgttgtggaa aatctggatc2100 attgacctct gtgctttcat tcctagagat gttttatagt tacatgagca aaagctgttg2160 ccccaaagtg atggccctgg aggcggggct gaggaacagg gaaatgccgc tgtgaagtct2220 taaagcactt ctgcttaaac tcccatgtgt gaggagtgtg cctccctgtg ccctctcagc2280 tctgaggctg gccgtctttc ggggtgttcc ttttggcaaa tatacactgt aatcttgagt2340 ctaaatttat atgttgaaat gctacctttt ttaaaataag aaactaaata aaattatttt2400 gaggggggg aggggaatgt ctcgagaggg ggggggtggg ggcgccgtcg agc

(2) INFORMATION ON SEQ ID NO. 77:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1962 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 - ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```
accgacggcc gccccttttc gtcttttttt tttttacatt tcaaatatat tttattactt 60
tccatcttag aaagaatatg aaacctgcat gcaatgctaa tggtttctga catgtacata 120
gcatataaca cagcagtaca atgcggcata tactgggggg cagtgtgtgg agggggggtt 180
cttaagggta tatgtacaga ggaaagggcg catggtcatc ttagctttcg aaagaggact 240
gcactgttta acattgaaga attacatggg gaatcacaaa tatattgctt tagtactgca 300
tgttctgttg tggtgaggga aagaaacatg ctttgaaggt tttcccttgt caacagaatg 360
tgtgtctgta gctgtgtatt gcgcatgtat tcatatattt ttaagttttc tcctaaggtt 420
tttgctgaca gtgttgggaa cctcacatgc ttctgaagca ttaaatattg aacctgtgaa 480
cctttcagaa atcctcaggt tgggaaagac cccacacctt ctttaaggat catttgtctc 540
gccatcacag gatcttggaa atgtttccta gggtgtgtaa aaattaacca ggggggaatg 600
aagcacattt ttctggcaac caaacttgag ttcctcagag aacagatgca gagagacctg 660
ctectgettg ceeggetaca ggggeeactg tggagteaca etgaggetgt gaeeggeeat 720
aaqcccagga gagcccgtgg cagctgtgcc gaggcgccag gacctctaag cggaaqcttc 780
ccaaqctagg aatggagcaa cactgcaatg aaatgtgtcc accaagctca ttgttcctcc 840
cgggcgctta taaagctcag atgtatagtg acgtatggac aaatacaaaa aaaaaaaaa 900
aaaaaaaaaa aaaaaaagcc tttcttctc acaggcataa gacacaaatt atatattgtt 960
atgaagcact ttttaccaac ggtcagtttt tacattttat agctgcgtgc gaaaggcttc1020
cagatqqqaq acccatctct cttqtqctcc aqacttcatc acaqqctqct ttttatcaaa1080
aaggggaaaa ctcatgcctt tcctttttaa aaaatgcttt tttgtatttg tccatacgtc1140
actatacatc tgagctttat aagcgcccgg gaggaacaat gagcttggtg gacacatttc1200
attgcagtgt tgctccattc ctagcttggg aagcttccgc ttagaggtcc tggcgcctcg1260
gcacagctgc cacgggctct cctgggctta tggccggtca cagcctcagt gtgactccac1320
agtggcccct gtagccgggc aagcaggagc aggtctctct gcatctgttc tctgaggaac1380
tcaagtttgg ttgccagaaa aatgtgcttc attccccct ggttaatttt tacacaccct1440
aggaaacatt tccaagatcc tgtgatggcg agacaaatga tccttaaaga aggtgtgggg1500
tettteccaa cetgaggatt tetgaaaggt teacaggtte aatatttaat getteagaag1560
catgtgaggt tcccaacact gtcagcaaaa accttaggag aaaacttaaa aatatatgaa1620
tacatgcgca atacacagct acagacacac attctgttga caagggaaaa ccttcaaagc1680
atgtttcttt ccctcaccac aacagaacat gcagtactaa agcaatatat ttgtgattcc1740
ccatgtaatt cttcaatgtt aaacagtgca gtcctctttc gaaagctaag atgaccatgc1800
geoettteet etgtacatat accettaaga acgeeecete cacacactge eccecagtag1860
tacgcaggca ttggtaccgg ctggtgttaa aatggctatg ggacatggtc aggaaaccat1920
ttaggcattg gcattgaggg ttccataatc cgtttctaag ga
                                                                 1962
```

- (2) INFORMATION ON SEQ ID NO. 78:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 788 base pairs
 - (B) TYPE: Nucleic acid(C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

cgttgcccc gccgggcg cgagatggat tccgggtgct ggttgttcgg cggcgagttc 60 gaggactcgg tgttcgagga gaggccggag cggcggtcag gaccgccgc gtcctactgc120 gccaagctct gcgagccga gtggtttat gaagaaacag aaagcagtga tgatgttgaa180 gtgctgactc tcaagaaatt caaaggagac ctggcctaca gacgacaaga gtatcagaaa240 gcactgcagg agtatccag agtatcctgaa aaattgcat caaccaattt tgccatgaaa300 agggatgtc aggaaggtca ggctcggtgt ctggctcacc tgggtaggca tatggaggcg360 ctggagattg ctgcaaactt ggaaaataaa gcaaccaaca cagaccattt aaccacggta420 ctgcagaaac tgattcttt gcatccttt aatccttgaa actggggcaa attggcagag540 gcttacctga atctggggca agctctttca gcatccttt gcagcacttg cgtcatctca gaaacagcac600 agtttcacct caagtgacaa aactatcaaa tccttcttc cacactcagg agaaatggca ggaaaattgg gaagttttgc aagtgcca acctggttgg aagggg780 acaggttt

- (2) INFORMATION ON SEQ ID NO. 79:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 299 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

aacctcctc gagggaattg atcttcagcc ctcccactc acaatctaca cagcagcctt 60 gaaggaaaag acgccagact tcagacgtct ctctcctcgc gtctcggaga ccgcggactc120 ccgtaaggtc gcccgtgggc cccgatttgt aatgcgggac aaccccgggc gcggggtga180 tcataggggt ctccaggcgc cggggtggat gaaggagggt cggggatggg ggggttttgta240 aaggggggctg tagaaggcg aaggaaggat gaaatttggg agggggggg gggggtcac 299

- (2) INFORMATION ON SEQ ID NO. 80:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2263 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

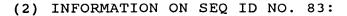
attacgacaa	ctcttctaca	tgtaagaaag	gaaaggtatt	ccctgggaag	atttcagtga	60
cagtatcaga	aacatttgac	ccagaagaga	aacattccat	ggcctatcaa	gacttgcata	120
gtgaaattac	tagcttgttt	aaagatgtat	ttggcacatc	tgtttatggá	cagactgtaa	180
ttcttactgt	aagcacatct	ctgtcaccaa	gatctgaaat	gcgtgctgat	gacaagtttg	240
ttaatgtaac	aatagtaaca	attttggcag	aaaccacaag	tgacaatgag	aagactgtga	300
ctgagaaaat	taataaagca	attagaagta	gctcaagcaa	ctttctaaac	tatgatttga	360
cccttcggtg	tgattattat	ggctgtaacc	agactgcgga	tgactgcctc	aatggtttag	420
catgcgattg	caaatctgac	ctgcaaaggc	ctaacccaca	gagccctttc	tgcgttgctt	480
ccagtctcaa	gtgtcctgat	gcctgcaacg	cacagcacaa	gcaatgctta	ataaagaaga	540
gtggtgggc	ccctgagtgt	gcgtgcgtgc	ccggctacca	ggaagatgct	aatgggaact	600
gccaaaagtg	tgcatttggc	tacagtggac	tcgactgtaa	ggacaaattt	cagctgatcc	660
tcactattgt	gggcaccatc	gctggcattg	tcattctcag	catgataatt	gcattgattg	720
tcacagcaag	atcaaataac	aaaacgaagc	atattgaaga	agagaacttg	attgacgaag	780
actttcaaaa	tctaaaactg	cggtcgacag	gcttcaccaa	tcttggagca	gaagggagcg	840
tctttcctaa	ggtcaggata	acggcctcca	gagacagcca	gatgcaaaat	ccctattcaa	900
gacacagcag	catgccccgc	cctgactatt	agaatcataa	gaatgtggaa	cccgccatgg	960
cccccaacca	atgtacaagc	tattatttag	agtgtttaga	aagactgatg	gagaagtgag1	.020
caccagtaaa	gatctggcct	ccggggtttt	tcttccatct	gacatctgcc	agcctctctg1	.080
aatggaagtt	gtgaatgttt	gcaacgaatc	cagctcactt	gctaaataag	aatctatgac1	140
attaaatgta	gtagatgcta	ttagcgcttg	tcagagaggt	ggttttcttc	aatcagtaca1	200
aagtactgag	acaatggtta	gggttgtttt	cttaattctt	ttcctggtag	ggcaacaaga1	.260
accatttcca	atctagagga	aagctcccca	gcattgcttg	ctcctgggca	aacattgctcl	.320
ttgagttaag	tgacctaatt	cccctgggag	acatacgcat	caactgtgga	ggtccgaggg1	.380
gatgagaagg	gatacccacc	acctttcaag	ggtcacaagc	tcactctctg	acaagtcagal	440
atagggacac	tgcttctatc	cctccaatgg	agagattctg	gcaacctttg	aacagcccag1	.500
agcttgcaac	ctagcctcac	ccaagaagac	tggaaagaga	catatctctc	agctttttca1	.560
ggaggcgtgc	ctgggaatcc	aggaactttt	tgatgctaat	tagaaggcct	ggactaaaaal	.620
tgtccactat	ggggtgcact	ctacagtttt	tgaaatgcta	ggaggcagaa	ggggcagaga1	
gtaaaaaaca	tgacctggta	gaaggaagag	aggcaaagga	aactgggtgg	ggaggatcaal	.740
ttagagagga	ggcacctggg	atccaccttc	ttccttaggt	cccctcctcc	atcagcaaag1	.800
gagcacttct	ctaatcatgc	cctcccgaag	actggctggg	agaaggttta	aaaacaaaaal	860
atccaggagt	aagagcctta	ggtcagtttg	aaattggaga	caaactgtct	ggcaaagggt1	.920
gcgagaggga	gcttgtgctc	aggagtccag	ccgtccagcc	toggggtgta	ggtttctgagl	980
gtgtgccatt	ggggcctcag	ccttctctgg	tgacagaggc	tcagctgtgg	ccaccaacac2	2040
acaaccacac	acacacaacc	acacacacaa	atgggggcaa	ccacatccag	tacaagcttt2	2100
tacaaatgtt	attagtgtcc	ttttttattt	ctaatgcctt	gtcctcttaa	aagttatttt2	160
atttgttatt	attatttgtt	cttgactgtt	aattgtgaat	ggtaatgcaa	taaagtgcct2	220
ttgttagatg	gtgaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaa		263
•						

- (2) INFORMATION ON SEQ ID NO. 81:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1284 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

aaaaatgggc taaactagct ccagagaact tgtgaattct ttgctaaagc ctctggcaaa aacggcattt gatgaagcaa ttgctgaatt ggatacgctg aatgaagagt cttataaaga 120 cagcactctg atcatgcagt tacttaggga caatctcact ctgtggacat cggaaaacca 180 gggagacgaa ggagacgctg gggagggaga gaactaatgt ttctcgtgct ttgtgatctg 240 ttcagtgtca ctctgtaccc tcaacatata tcccttgtgc gataaaaaaa aaaaaaaaa 300 aaaaaagagt cgtacgtcga ctttcgattt ttcacagcct cagcctagga aaaatggttc 360 atgggataaa cagctggtat ttgtatctaa aactcagatt ggtcacataa atgccacggc 420 attocgaagt tttgattttg attaacattg acaggattac tgtgtgttta attttttaaa 480 aactgaacac tgtgattatg gggttttgta atttagcaga actcttactg gtagaaaaaa 540 tagacctgaa ttatgtgtaa ctttttggaa ggtttaatct gatatcaaaa taatcattga 600 aatacaattc cattgtaaag ttgtacagaa agttatagag attatattgt gatgctggaa 660 cttggagtga gacacacatc atttggcatt tgagttgaat ggtaattcac agtaatgctg 720 ccgttgttcg ggacttaaag acacttgacc tgtttgggct gttgccactt aaaagttcat 780 gaccacaaat gtccacagtg tcttcctctg aggaaactcg aatcctgaaa tggaaattct 840 ttgtggcaga taactggctt atgacacctt gaaaagttca agtgctcata taacacacca 900 cactgaaccc cctttcctac agcaatatgt tcactatgtt accaatttgc aacttgtgct 960 tcaatagtgg aatctacttt cattgttaac actgagctaa agaaaaaaag ccgtgtgttt1020 tatgaatgac cttatctgtt tcctggataa tacctttaag aataatgtcc tgagtcaggc1080 gtggtggtgc gtgcatctag tcccaactat ttgggaggct gaggcaggag gatcgcttgal140 gcccaggagt ttaaagctgc agtgccctgt ggttgcacct gtgaataact gcactccagc1200 ctgggcaaca tagcgagacc tcatctccaa aaaagaaaaa aacacaaaag gatgtgtctg1260 taagaggctt ccctggggga ccag

- (2) INFORMATION ON SEQ ID NO. 82:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1335 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```
gggtgacata atgacaggtt aaatatttgt gattcattga ttaaatatta tttaaagaaa 60
tgtaaattca caataagggt tgaaaattat ttggtttcat ccattgtctc ttatttcagg 120
accaagcage aaactgcagt agtttgtgaa ggattctaat atggggttca ggaatageet 180
ctcaacgcta ctaattcaga tctctcccag agaactactg gatttcctca taattgacaa 240
acatgagtga ccacctettt gggtggetac tgttagaaat ggctgttgtc atgttttetg 300
gactttgcca gccaacagat ccctgccagg ttttggaaat acttctatta cctcgctgct 360
acttttctgc agggataaaa cttttgaggt ggccagaccc agaacatcca aggattcctg 420
ttacagtgct acagtataca ctgctcattt atcctattct catgtgcttt cttctttagt 480
aagattattt taagaaaata agtgatattt aaagtccaaa gaggaatgat cacagttgta 540
taaggggtgt tttcccactt gaactctgat gtcagtcgac tgtgggtcag agctacaacc 600
atctgtttgg tttgatgttt tggtggttta cttacggagt ggggatagtg tgagacctaa 660
ttccctgtgc aaatgtctct tattccagaa atgtgcattt tgtcatctat aagcaagaaa 720
tatgggcata gcagctcttg gtttaaagtt tgccataacc tgttcatgtt tgttttaagc 780
tcaggtaaag ataacctcct ctttctatga ctccagtttc cattcaggtt atagtattat 840
tcaatagttg attitctitt taagctgggc aataaattga tgtttccaga tggtaacatg 900
ggagagggca tataggataa agatgagcaa attctaccct aaaaatgttc tagtagttca 960
caggaagaag atgaggttta ataactttca aggtaattct agattgacat tttgagggga1020
aaatgggctc ttgttctagt tgaagtgagc agagaaggct ataaattaat atgtaactta1080
cagcattcca gaggttaaaa ataactgatg cagatgtact tcttcagtgt gattcttcag1140
atcaaacttt tacttttggc atagttaatt tcagaaaaat gtgctgtatg tgtgtgtgta1200
tgagggttgg tcttgctgat ccttcagtta gctctaaatt ctggcaactc cttgtaattc1260
ccatgtattt gataccatga accaatcatg ttgaatgcgt ttggtgatct ggggagcctc1320
ccccgtcttc ccagg
```



(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1890 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

ggcttgtggc ggctctgcca caggggcagg tgttgagggg ctcccggtcc ggctgccgcc 60 getecceege teeggaceeg gggeteccee tagegeeget gaggageege etetgeggte 120 caggagggcg caggagcggg actgagagcg cctggaggct cgagcagagg atagaaggac 180 aaqqacaqaa tcaccagcac tggctgaagg taccttaaca tggggaatct tcttaaagtt 240 ttgacatgca cagacettga geaggggeea aatttttee ttgattttga aaatgeeeag 300 cctacagagt ctgagaagga aatttataat caggtgaatg tagtattaaa agatgcagaa 360 ggcatcttgg aggacttgca gtcatacaga ggagctggcc acgaaatacg agaggcaatc 420 cagcatccag cagatgagaa gttgcaagag aaggcatggg gtgcagttgt tccactagta 480 ggcaaattaa agaaatttta cgaattttct cagaggttag aagcagcatt aagaggtctt 540 ctgggagcct taacaagtac cccatattct cccacccagc atctagagcg agagcaggct 600 cttgctaaac agtttgcaga aattcttcat ttcacactcc ggtttgatga actcaagatg 660 acaaatcctg ccatacagaa tgatttcagc tattatagaa gaacattgag tcgtatgagg 720 attaacaatg taccggcaga aggagaaaat gaagtaaata atgaattggc aaatcgaatg 780 tctttgtttt atgctgaggc aactccaatg ctgaaaacct tgagtgatgc cacaacaaaa 840 tttgtatcag agaataaaaa tttaccaata gaaaatacca cagattgttt aagcacaatg 900 gctagtgtat gcagagtcat gctggaaaca ccggaataca gaagcagatt tacaaatgaa 960 qaqacaqtqt cattctgctt gagggtaatg gtgggtgtca taatactcta tgaccacgta1020 catccagtgg gagcatttgc taaaacttcc aaaattgata tgaaaggttg tatcaaagtt1080 cttaaqqacc aacctcctaa tagtgtggaa ggtcttctaa atgctctcag gtacacaaca1140 aaacatttga atgatgagac tacctccaag caaattaaat ccatgctgca ataacaattc1200 tggaataagc acctgctgta gacagaagac agtattctgc aatgactgag aatgcagttt1260 tttagtgatt gcaattacta tctcatttat tcttgctttt atttctttcc tctgttcctc1320 ttccctcttt tttaatcatg ttcttaagac ttcttttctg tgccaaaatc agtaaagtta1380 cactetgaag ggatateate ettteaaaeg ggecatetaa ggeagetaat tatgeattge1440 attggggtct ctactgagaa aaattctgtg acttgaacta aatattttta aatgtggatt1500 ttttttgaaa ctaatattta atattgcttc tcctgcatgg caaaactgcc tattctgcta1560 tttaaaaacc ctcaatgact ttattttcta ctgccgcctt tttcatgtgc aaccaaaatg1620 aaaatgttta aattaactgt gttgtacaaa tggtacccaa cacaaacttt ttttaaatta1680 gtaatacttt tgtttaaagt tttaagtttg cattttgact ttttttgtaa ggatgtatgt1740 tgtgtgttta acctttatta actaacgtta aaagctgtga tgtgtgcgta gaatattacg1800 tatgcatgtt catgtctaaa gaatggctgt tgatgataaa ataaaaatca gctttcattt1860 1890 ttctaaaaaa aaaaaaaaaa aaaaaaaaaa

- (2) INFORMÁTION ON SEQ ID NO. 84:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1829 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```
gaccaacctg acgcagatcg agctgcgggg caaccggctg gagtgcctgc ctgtggagct
gggcgagtgc ccactgctca agcgcacggc ttggtggtgg aggaggacct gttcaacaca 120
ctgccacccg aggtgaagga gcggctgtgg agggctgaca aggagcaggc ctgagcgagg 180
ccggcccagc acagcaagca gcaggaccgc tgcccagtcc tcaggcccgg aggggcaggc 240
ctagettete ecagaactee eggacageca ggacageete gtggetggge aggageetgg 300
ggccgcttgt gagtcaggcc agagcgagag gacagtatct gtggggctgg ccccttttct 360
ccctctgaga ctcacgtccc ccagggcaag tgcttgtgga ggagagcaag tctcaagagc 420
gcagtatttg gataatcagg gtctcctccc tggaggccag ctctgcccca ggggctgagc 480
tgccaccaga ggtcctggga ccctcacttt agttcttggt atttatttt ctccatctcc 540
cacctccttc atccagataa cttatacatt cccaagaaag ttcagcccag atggaaggtg 600
ttcagggaaa ggtgggctgc cttttcccct tgtccttatt tagcgatgcc gccgggcatt 660
taacacccac ctggacttca gcagagtggt ccggggcgaa ccagccatgg gacggtcacc 720
cagcagtgcc gggctgggct ctgcggtgcg gtccacggga gagcaggcct ccagctggaa 780
aggccaggcc tggagcttgc ctcttcagta tttgtggcag ttttagtttt ttgtttttt 840
ttttttaatc aaaaaacaat ttttttaaaa aaaaaagctt tgaaaatgga tggtttgggt 900
attaaaaaga aaaaaaaac ttaaaaaaaa aaagacacta acggccagtg agttggagtc 960
tcagggcagg gtggcagttt cccttgagca aagcagccag acgttgaact gtgtttcctt1020
tecetgggeg cagggtgeag ggtgtettee ggatetggtg tgacettggt ceaggagtte1080
tatttgttcc tggggaggga gttttttttg gtgtcttgtt ttctttctcc tccatgtgtc1140
ttggcaggca ctcatttctg tggctgtcgg ccagagggaa tgttctggag ctgccaagga1200
gggaggagac tcgggttggc taatccccgg atgaacggtg ctccattcgc acctccctc1260
ctcgtgcctg ccctgcctct ccacgcacag tgttaaggag ccaagaggag ccacttcgcc1320
cagactttgt ttccccaccg cctgcggcat gggtgtgtcc agtgccaccg ctggcctccg1380
ctgcttccat cagccttgtc gccacctggt ccttcatgaa gagcagacac ttagaggctg1440
qtcqqqaatq qqqaqqtcqc ccctqqqaqq qcaqqcqttq qttccaaqcc qqttcccqtc1500
cctqqcqcct ggagtgcaca cagcccagtc ggcacctggt ggctggaagc caccctgctt1560
tagatcactc gggtccccac cttagaaggg tccccgcctt agatcaatca cgtggacact1620
aaggcacgtt ttagagtctc ttgtcttaat gattatgtcc atccgtctgt ccgtccattt1680
gtgttttctg cgtcgtgtca ttggatataa tcctcagaaa taatgcacac tagcctctgal740
caaccatgaa gcaaaaatcc gttacatgtg ggtctgaact tgtagactcg gtcacagtat1800
caaataaaat ctataacaga aaaaaaaaa
```

- (2) INFORMATION ON SEQ ID NO. 85:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2358 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

cgaaacgccg	cggagtgagg	cagttccgct	ggctagtgtg	tacgcggcga	gcttctcccg	60
gcgccgcccg	ctcggctccc	atagegeeeg	cgacagggtc	cggacgccgc	ccgaacatgg	120
actccgccgg	ccaagatatc	aacctgaatt	ctcctaacaa	aggtctgctg	tctgactcca	180
tgacggatgt	tcctgtcgac	acaggtgtgg	ctgcccggac	tcctgctgtt	gagggtctga	240
cagaggctga	ggaggaggag	ctcagggctg	agcttaccaa	ggtggaagag	gaaattgtca	300
ctctgcgcca	ggtcctggca	gccaaggaga	ggcactgtgg	agagctcaag	aggaggctgg	360
gcctctccac	cctgggggag	ctgaaacaga	acctgtccag	gagctggcat	gacgtgcagg	420
		acttctgaga				480
agtcagacct	ctacaagaag	actcaggaaa	ctctttcaca	ggcaggacag	aagacttcag	540
ctgccctgtc	cacagtgggc	tctgccatca	gcaggaagct	tggagacatg	aggaactctg	600
		gaccgagttg				660
gagagaacgg	cagtgacaac	ctcccttcct	cagcggggag	tggtgacaag	cccctgtcgg	720
		tgtggttgct				780
		tctgttcagc				840
		gcccatccac				900
		acacagatgt				960
cactgtgctg	tccttcctag	gggtgcagga	agtggacagg	gcggagggtt	tgaaagaata1	L020
		cctttgggaa				
tgaagagttc	taagcataaa	ataagtggca	ttttctgact	tcttcctcct	cctccttccc1	1140
tgactcacag	aaggaatgca	atcacccagc	aagtcctacc	tgttacgcaa	ttttttatct1	L200
		ctgtccattt				
cagcagctgc	ctgattgtta	cgcgaatcta	gctttaacgg	aagcaaattc	attattttt1	L320
		aaagtttaaa				
		ctgaaataca				
tctaatttt	atatgtatat	agatgagggt	tccttaatgg	ttgtgagcat	tgtgtggaat!	1500
tttacacctg	gcctgcgtgg	cagcctcttc	cagttgaggt	gttttatgtc	acgcacactc1	1560
catcccagtg	tacaaaacct	gcttctcttc	tcaaccgtgg	cagctcccgc	tggctcctat	1620
gccctgccct	aaagggctct	tgagcctctg	ggaatgggag	gggccaagag	aaggaaaacci	1680
ctgtctttag	caccctttaa	aagaactgtg	cccccttct	cagtgctgcc	tttgcatggg:	1740
cctggcccgg	ctcgcattcg	tcagtgactc	caaccctcct	gcttgctgta	cttgggatga:	1800
	caggtcaggt			cagccaggat		
gtctttttct	caggagctac	aaagatctct	tcctgttact	aaatggtcgc	accccagcag:	1920
cctctctcgc	acaccggggc	cctgcatgtc	agatggcgtg	gtctgcaggg	ggagctctgt?	1980
gccttagtgg	ctcttggcag	gacactgagg	gcctgcctgt	ggtgtgcccg	gctctgccac	2040
		ctcagctcaa				
		agttcagaca				
		cccagcgctc				
		caggttgtgc				
gttattataa	taatgggtaa	tttgtcaata	aagcattect	ttgggggaaa	aaaaaaaaa	2340
aaaaaaaaa			,			2358
•		•		_		

- (2) INFORMATION ON SEQ ID NO. 86:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1646 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO.
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```
cagctgcgga actgcgcgat tgtggttccc gccgtatttc ccgttcccca tctagtaact
cccatctcag cccacgtatc tccctgagtg gaaatctcgg gccccagacc agtcgattgg 120
gaggtccgcc ctccccttca gcgacttggt ctgtgttttg gcagttgccg cgacaacagt 180
cacttccggg aagggggtct gcgaatctcc ttccgtcggt ccgctcagaa tcaqctqtcc 240
teteagactg tgtgggtggt tteeceggee geageteegt aegggettgg attgetggge 300
ctcggtgcac cccagcctcc cccactcggg ttctgagctt gagctggcgg ctctttaact 360
ctgcttcact gttgctcttg gcaacatcca cttccgggag cgagtgccgt ttcccccgct 420
caccgcgggc tagggagcgt gggattccgg actgtgagcg gctgttagtg cgtcgcagct 480
getggegate eggegaeeet eggeeggeag gaeeegeggg ceaegeagee ggggeettet 540
caacgcctca gtacctcggc gggaccgcca tggttctgct gcacgtgaag cggggcgacg 600
agagecagtt cetgetgeag gegeetggga gtacegaget ggaggagete aeggtgeagg 660
tggcccgggt ctataatggg cggctcaagg tgcagcgcct ctgctcagaa atggaagaat 720
tagccgaaca tggcatattt ctccctccta atatgcaagg actgaccgat gatcagattg 780
aagaattgaa attgaaggat gaatggggtg aaaaatgcgt acccagcgga ggtgcagtgt 840
ttaaaaagga tgatattgga cgaaggaatg ggcaagctcc aaatgagaag atgaagcaag 900
tgttaaagaa gactatagaa gaagccaaag caataatatc taagaaacaa gtggaagccg 960
gtgtctgtgt taccatggag atggtgaaag atgccttgga ccagcttcga ggcgcggtga1020
tgattgttta ccccatgggg ttgccaccgt atgatcccat ccgcatggag tttgaaaata1080
aggaagactt gtcgggaaca caggcagggc tcaacgtcat taaagaggca gaggcgcactll40
gtggtgggca gccaaggagc tgagaagaac gaagaagctt tcagactacg tggggaagaa1200
tgaaaaaacc aaaattatcg ccaagattca gcaaagggga cagggagctc caqcccqaqa1260
gcctattatt agcagtgagg agcagaagca gctgatgctg tactatcaca gaagacaaga1320
ggagctcaag agattggaag aaaatgatga tgatgcctat ttaaactcac catgggcgga1380
taacactgct ttgaaaagac attttcatgg agtgaaagac ataaagtgga gaccaagatg1440
aagttcacca gctgatgaca cttccaaaga gattagctca cctttctcct aggcaattat1500
aatttaaaaa aaaaaaaag gccacttact gccctctgta aaagatgtta acatttctag1560
ttttctttta gtgtgaattt ttaaaatagc agttattcaa ggttttagaa cttaataaat1620
acctagtcag aagaaaaaaa aaaaaa
                                                                 1646
```

(2) INFORMATION ON SEQ ID NO. 87:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3096 base pairs
 - (B) TYPE: Nucleic acid. (C) STRAND: individual

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

gcgggtgacg	cgacgacggc	tcgacacttt	gctacggagt	gcatcggacg	tcgaagccta 60
gagtetetge	gtctttccct	cttccgctgc	ctcattcctt	tccttcctag	ccttagtcgt 120
cgccgccacc	atgaacaaga	agaagaaacc	gttcctaggg	atgcccgcgc	ccctcggcta 180
caraccadad	cradaccada	gcgccactgg	cttcaccacq	cggtcagaca	ttgggggggg 240
ccgtgatgca	aatgaccctg	tggatgatcg	ccatgcaccc	ccaggcaaga	gaaccottoo 300
ggaccagatg	aagaaaaatc	aggctgctga	cgatgacgac	gaggatctaa	atgacaccaa 360
ttacgatgag	tttaatggct	atgctgggag	cctcttctca	agtggaccct	acgagaaaga 420
tgatgaggaa	gcagatgcta	tctatgcagc	cctggataaa	aggatggatg	aaagaagaaa 480
agaaagacgg	gagcaaaggg	agaaagaaga	aatagagaaa	tatcqtatqq	aacgccccaa 540
aatccaacag	cagttctcag	acctcaagag	gaagttggca	gaagtcacag	aagaagagtg 600
getgageate	cccgaggttg	gcgatgccag	aaataaacgt	caqcqqaacc	cacgctatga 660
gaagetgace	cctgttcctg	acagtttctt	tgccaaacat	ttacagaccg	gagagaacca 720
tacctcagtg	gateceegae	aaactcaatt	tggaggtctt	aacacaccct	atccaggtgg 780
actaaacact	ccatacccag	grggaargac	gccaggactg	atgacacctg	gcacagtgag 840
ctggacatga	ggaagattgg	ccaagcgagg	aacactctga	tggacatgag	gctgagccag 900
grgrcrgact	ccgtgagtgg	acagaccgtc	gttgacccca	aaggctacct	gacggattta 960
aattccatga	tcccgacaca	cggaggagac	atcaatgata	tcaagaaggc	gcgactgctc1020
ctcaagtctg	ttcgggagac	gaaccctcat	cacccgccag	cctggattgc	atcagccccc1080
ctggaagaag	tcactgggaa	gctacaagta	gctcggaacc	ttatcatgaa	ggggacggag1140
atgtgcccca	agagtgaaga	tgtctggctg	gaagcagcca	ggttgcagcc	tggggacaca1200
gccaaggccg	tggtagccca	agctgtccgt	catctcccac	agtctgtcag	gatttacatc1260
agagccgcag	agctggaaac	ggacattcgt	gcaaagaagc	gggttcttcg	gaaagccctc1320
gagcatgttc	caaactcggt	tegettgtgg	aaagcagccg	ttgagctgga	agaacctgaa1380
gatgctagaa	tcatgctgag	ccgagctgtg	gagtgctgcc	ccaccagcgt	ggagctctgg1440
crederergg	caaggctgga	gacctatgaa	aatgcccgca	aggtcttgaa	caaggcgcgg1500
gagaacattc	ctacagaccg	acatatctgg	atcacggctg	ctaagctgga	ggaagccaat1560
gggaacacgc	agatggtgga	gaagatcatc	gaccgagcca	tcacctcqct	gcgggccaac1620
ggtgtggaga	tcaaccgtga	gcagtggatc	caggatgccg	aggaatgtga	cagggctggg1680
agtgtggcca	cctgccaggc	cgtcatgcgt	gccgtgattg	ggattgggat	tgaggaggaa1740
gatcggaagc	atacctggat	ggaggatgct	gacagttgtg	tagcccacaa	tgccctggag1800
cgcgcacgag	ccatctacge	ctacgccctg	caggtgttcc	ccagcaagaa	gagtgtgtgg1860
cracacacca	cgtacttcga	gaagaaccat	ggcactcggg	agtccctqqa	agcactcctg1920
cagagggctg	tggcccactg	ccccaaagca	gaggtgctgt	ggctcatqqq	cgccaagtcc1980
aagtggctgg	caggggatgt	gcctgcagca	aggagcatcc	tggccctggc	cttccaggcc2040
aaccccaaca	gtgaggagat	ctggctggca	gccgtgaagc	tggagtccga	gaatgatgag2100
tacgagcggg	cccggaggct	gctggccaag	gcgcggacag	tgcccccacc	gcccgggtgt2160
tcatgaagtc	tgtgaagetg	gagtgggtgc	aagacaacat	cagggcagcc	caagatctgt2220
gcgaggaggc	cctgcggcac	tatgaggact	tccccaaget	gtggatgatg	aaggggcaga2280
ccgaggagca	gaaggagatg	atggagaagg	cgcgggaagc	ctataaccag	gggttgaaga2340
agtgtcccca	ctccacacec	ctgtggcttt	tgctctctcg	gctggaggag	aagattgggc2400
agettaeteg	agcacgggcc	attttggaaa	agtctcgtct	gaagaaccca	aagaaccctg2460
ggetgtggtt	ggagtccgtg	cggctggagt	accgtgcggg	gctgaagaac	atcgcaaata2520
cactcatggc	caaggcgctg	caggagtgcc	ccaactccgg	tatcctgtgg	tctgaggcca2580
					•
cctcctcga	ggcaaggccc	cagaggagga	.ccaagagcgt	ggatgccctg	aagaagtgtg2640
agcatgaccc	ccatgtgctc	ctggccgtgg	ccaagctgtt	ttggagtcag	cogaagatca2700
ccaaggccag	ggagtggttc	caccgcactg	tgaagattga	ctcggacctg	agagatacet2760
gggccccccc	Cladagttt	gagctgcagc	atggcactga	ggaggaggag	gaggaggtga2820
ggaagegeeg	cyayaycyca	gageetegge	atqqqqaqct	ataatacacc	atatacaaaa2880
acaccyccaa	ccggcagaag	aagatcgggg	acatccttag	actaataacc	ggccgcatca2940
ayaacacccc	Cigatigage	ggttgccatg	gccggtctcc	ataaaacaaa	attagaccac3000
argrygaagg	getetgaget	grgreetect	tcattaaaag	tttttatgtc	tcgtgtcaga3060
aaaaaaaya	aaagaaaaa	aaaaacaccc	ggggc		3096

(2) INFORMATION ON SEQ ID NO. 88:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1906 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```
gegetegetg aggeaagagg agggeacteg geogeggeet gacagggaet tageceacag 60
 agaccygccc gcgcgcgcga ccccacaccc acccactcgt ccacctaccc actccccgcg 120
 ccgcctcctc ccaccctgag cagagccacc gaggatgata aacacccagg acagtagtat 180
 tttgccgttg agtaagtgtc cccagctcca gtgctgcagg cacattgttc cagggcctct 240
gtggtgctcc tgatgcccct cacccactgt cgaagatccc cggtgggcga gggggcgac 300
 gggatcette teteteaget etaatatata aggaegagaa geteaetgtg acceaggace 360
tecetytyaa tyatyyaaaa eeteacatey teeaetteea ytatyayyte accyayytya 420
 aggiciette tigggatgea gicetgicea gecagageet gittgiagaa ateccagatg 480
 gattattagc tgatgggagc aaagaaggat tgttagcact gctagagttt gctgaagaga 540
 agatgaaagt gaactatgtc ttcatctgct tcaggaaggg ccgagaagac agagctccac 600
 tectgaagae etteagette ttgggetttg agattgtaeg tecaggeeat ecetgtgtee 660
 ceteteggee agatgtgatg tteatggttt ateceetgga ecagaacttg teegatgagg 720
 actaatagtc atagaggatg ctttacccaa gagccacagt gggggaagag gggaagttag 780
 gcagccctgg gacagacgag agggctcctc gctgtctagg gaaggacact gaggggctca 840
 gggtgagggt tgcctattgt gttctcggag ttgactcgtt gaaattgttt tccataaaga 900
 acagtataaa catattatto acatgtaato accaatagta aatgaagatg tttatgaact 960
 ggcattagaa gctttctaaa ctgcgctgtg tgatgtgttc tatctagcct aggggaggac1020
 attgcctaga gggggaggga ctgtctgggt tcaggggcat ggcctggagg gctggtgggc1080
 agcactgtca ggctcaggtt tccctgctgt tggctttctg ttttggttat taagacttgt1140
 gtattttctt tctttgcttc ctgtcacccc aggggctcct gagtataggc ttttcagtcc1200
 ctgggcagtg tccttgagtt gttttttgac actcttacct gggcttctct gtgtgcattt1260
 gegtetggee tggagtaage aggteegaee eeteettett tacagettag tgttattetg1320
 gcatttggtt aagctggctt aatctgttta atgttatcag tacattttaa ataggggcat1380
tgaaatttac tcccaccacc agggcttttt tgggggatgc ctgggccttt aaaacactag1440
ccaaactcta attaattctc aaatcactgc caggagttct tgctcctggc tgcaggccca1500
qqccccaagg tctccttctt ggggtcacaa acagcagtaa ggaagaggaa tatatagcaa1560
ctcaqqqcct gggaattgtg gggcaatccg ttcttaggga ctggatactt ctggctggct1620
gagtatagta ctagetgeet ecceaceagg tteegagtag tgtetgagae tetgetetge1680
agggcctagg gtagcgctgg gagtgtagaa gtggcctgcc cttaactgtt ttcactaaac1740
agetttttet aaggggagag caagggggag agatctagat tgggtgaggg ggacggggat1800
qtcaqqqaqq caaqtqtqtt qtqttactqt qtcaataaac tqatttaaaq ttqtaaaaaa1860
aaaagaaagg gggggggtgg aggggaggga gggggaaaag aaaaaa
```

- (2) INFORMATION ON SEQ ID NO. 90:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

gctaagagga caagatgagg cccggcctct catttctcct agcccttctg ttcttccttg 60 gccaagctgc aggggatttg ggggatgtgg gacctccaat tcccagcccc ggcttcagct120 ctttcccagg tgttgactcc agctccagct tcagctccag ctccaggtcg ggctccagct180 ccagccgcag cttaggcagc ggaggttctg tgtcccagtt gttttccaat ttcaccggct240 ccgtggatga ccgtggacc tgccagtgct ctgtttccct gccagacaac aactttcccg300 tggaccagagt ggaacgttgg aattcacagc tcatagttat ttctcagag 349

- (2) INFORMATION ON SEQ ID NO. 91:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2142 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN .
 - (C) ORGAN:

(vii) OTHER ORIGIN: (A) LIBRARY: cDNA library

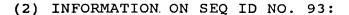
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

cagacccaga	aagtagtgac	cagccctcct	cggattaccc	ttcattggct	cctcccttgc	60
gccgcccacc	ctccagattt	gcataaaaaa	ggccaagaaa	actctggctg	tgccccagca	120
acggctcatt	ctgctccccc	gggtcggagc	ccccggagc	tgcgcgcggg	cttgcagcgc"	180
ctcgcccgcg	ctgtcctccc	ggtgtcccgc	ttctccgcgc	cccagccgcc	ggctgccagc	240
ttttcggggc	cccgagtcgc	acccagcgaa	gagagcgggc	ccgggacaag	ctcgaactcc	300
ggccgcctcg	cccttccccg	gctccgctcc	ctctgccccc	tcggggtcgc	gcgcccacga	360
				ctcgcactgc		420
cggcgcgcgg	gctcttcctc	tttggccagc	ccgacttctc	ctacaagcgc	agaattgcaa	480
gcccatcccg	gccaacctgc	agctgtgcca	cggcatcgaa	taccagaaca	tgcggctgcc	540
caacctgctg	ggccacgaga	ccatgaagga	ggtgctggag	caggccggcg	cttggatccc	600
gctggtcatg	aagcagtgcc	acccggacac	caagaagttc	ctgtgctcgc	tcttcgcccc	660
cgtctgcctc	gatgacctag	acgagaccat	ccagccatgc	cactcgctct	gcgtgcaggt	720
gaaggaccgc	tgcgccccgg	tcatgtccgc	cttcggcttc	ccctggcccg	acatgcttga	780
gtgcgaccgt	ttcccccagg	acaacgacct	ttgcatcccc	ctcgctagca	gcgaccacct	840
cctgccagcc	accgaggaag	ctccaaaggt	atgtgaagcc	tgcaaaaata	aaaatgatga	900
tgacaacgac	ataatggaaa	cgctttgtaa	aaatgatttt	gcactgaaaa	taaaagtgaa	960
ggagataacc	tacatcaacc	gagataccaa	aatcatcctg	gagaccaaga	gcaagaccat!	1020
				tcggtgctgt		
cagcttgcag	tgcacctgtg	aggagatgaa	cgacatcaac	gcgccctatc	tggtcatggg:	L140
acagaaacag	ggtggggagc	tggtgatcac	ctcggtgaag	cggtggcaga	aggggcagag:	1200
agagttcaag	cgcatctccc	gcagcatccg	caagctgcag	tgctagtccc	ggcatcctga:	1260
tggctccgac	aggcctgctc	cagagcacgg	ctgaccattt	ctgctccggg	atctcagctc:	1320
ccgttcccca	agcacactcc	tagctgctcc	agtctcagcc	tgggcagctt	cccctgcct:	1380
tttgcacgtt	tgcatcccca	gcatttcctg	agttataagg	ccacaggagt	ggatagctgt:	1440
tttcacctaa	aggaaaagcc	cacccgaatc	ttgtagaaat	attcaaacta	ataaaatcat:	1500
				tagttttgaa		
tgtgacttgg	gtctggttgg	ttgttgtttg	ttgttttgag	tcagctgatt	ttcacttccc	1620
				tgtggcccaa		
				tcttcatcag		
				accttcaatg		
				attagaagca		
ttctatagca	tgatttcttc	aagtaaaagg	caaaagatat	aaattttata	attgacttga	1920
				tgcaaattaa		
				gtaaaaatat		
				ataaacttta		
tacctataaa	aaaaaaaaa	aaaaaaaaa	aaaaaaggg	aa		2142

(2) INFORMATION ON SEQ ID NO. 92:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1111 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```
cgtgggcgaa catgggagct gttcctcgcg ggccgccggg tgctggtcac cggggcaggc 60
aaaggtatag ggcgcgcac ggtccaggcg ctgcacgcga cgggcgcgcg ggtggtggct 120
gtgagccgga ctcaggcgga tcttgacagc cttgtccgcg agtgcccggg gatagaaccc 180
gtgtgcgtgg acctgggtga ctgggaggcc accgagcggg cgctgggcag cgtgggcccc 240
gtggacctgc gcggagactg cgccgacatg gagctgttcc tcgcgggccg ccgggtgctg 300
gtcaccgggg caggcaaagg tatagggcgc ggcacggtcc aggcgctgca cgcgacgggc 360
gegegggtgg tggetgtgag ceggacteag geggatettg acageettgt cegegagtge 420
ccggggatag aacccgtgtg cgtggacctg ggtgactggg aggccaccga gcgggcgctg 480
qqcaqcqtqq gccccqtqqa cctqctqqtq aacaacqccq ctqtcqccct gctqcaqccc 540
ttcctggagg tcaccaagga ggcctttgac agatcctttg aggtgaacct gcgtgcggtc 600
atccaggtgt cgcagattgt ggccaggggc ttaatagccc ggggagtccc aggggccatc 660
gtgaatgtet ecagecagtg eteceagegg geagtaacta accatagegt etactgetee 720
accaagggtg coctggacat gotgaccaag gtgatggccc tagagetegg geoccacaag 780
atcogagtga atgcagtaaa coccacagtg gtgatgacgt ccatgggcca ggccacctgg 840
agtgacccc acaaggccaa gactatgctg aaccgaatcc cacttggcaa gtttgctgag 900
gtagageacg tggtgaacge catectett etgetgagtg acegaagtgg catgaceacg 960
ggttccactt tgccggtgga agggggcttc tgggcctgct gagctccctc cacacctc1020
aagccccatg ccgtgctcat cctaccccca atccctccaa taaacctgat tctgctgccc1080
aaaaaaaaa aaaaaaaaa aaaaaaaaa g
                                                                 1111
```



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 657 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

atttaaagcc tggattgtaa ccagattttc tttttcccc cttctcagct gtagatatga 60 tatctccttt cagggcccca gcttaagggc aaagtgagtt aatgtgtaga caaaggcgag120 ggacaagaga gagttaacat ctagacagtg gaaaaagcca tggtgtgtgg tttctgggaa180 ccaccaacac ttgcaggttt agcttttcc cagggttgac tacaagaaag aaaaccatgt240 ttttgcaaga ttaaaatgtg gttgagtgtg cctaaattaa ccatccccat ttttatcata300 tttccaccat cacttcaggg ttttaagagt cagtgctcac ctgggcggac tggtagtaca360 ttttgcttct tagaaagcta agtcctgggt tccgtctgat tttaggttcc aggaacttcc420 tgagaacacc cgatcgcaga gggtaatttt ctggagtttg ttttgcaggg atagctgga480 gtatggccac cctgctccac gatgcggtaa tgaatccagc agaagtggtg aagcagcgct540 tgcagatgta caactcgcag caccggtcag caaccacgcc gagccctatc tcgtgcc 657

- (2) INFORMATION ON SEQ ID NO. 94:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 863 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

gcggtcggta gtgcggcgt gtttaaagat ggcggcggag gaacctcagc agcagaagca 60 ggagccgctg ggcagcgact ccgaaggtgt taactgtctg gcctatgatg aagccatcat120 ggctcagcag gaccgaattc agcaagagat tgctgtgcag aaccctctgg tgtcagagcg180 gctggagctc tcggtcctat acaaggagta tgctgaagat gacaacatct atcaacagaa240 gatcaaggac ctccacaaaa agtactcgta catccgcaag accaggcctg acggcaactg300 ttctatctgg gctttcggat tctcccactt ggaggcactg ctggatgaca gcaaggagtt360 gcagcggttc aaggctgtgt ctgccaagag caaggagacact ctggatgaca agggcttcac420 tgaattcaca attgaggatt tccacacac gttcatgac ctgattgac aggtggagaa480 gcagacctct gtcgcgacc tgctggccc cttcaatgac cagagcacct ccgactacct540 tgtggtctac gagggtggac ggactgtcaa ggagttctgc cagcaggaga agttcttcga600 gtgcaaggag agcgaccaca tccacatcat tgcgctgcc cagcagagag tggagcccat660 gtgcaaggag gaccgaccac tccacatcat tgcgctgcc cagcacaca tcttccctga780 ggccttccga gcccaaggtc ttaaccttgtt ttaaccaca tggggcaatt tagggtattg840 tttttacaaa taggggtttg gtt

- (2) INFORMATION ON SEQ ID NO. 95:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1015 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

aattoggaac gagggogoot gcaagcoatg atgaccoaco tgcatgtgaa gtotacagaa 60 cccaaagctg cccctcagcc cctgaatctg gtatcaagtg tcaccctctc caagtccgca 120 teggaggett etecacagag ettaceteat actecaacga ecceaacege ecceetgact 180 cocgtcaccc aaggcccctc tgtcatcaca accaccagca tgcacacggt gggacccatc 240 cgcaggcggt actcagacaa atacaacgtg cccatttcgt cagcagatat tgcgcagaac 300 caagaatttt ataagaacgc agaagttaga ccaccattta catatgcatc tttaattagg 360 caggocatto togaatotoo agaaaagoag otaacactaa atgagatota taactggtto 420 acacgaatgt ttgcttactt ccgacgcaac gcggccacgt ggaagaatgc agtgcgtcat 480 aatcttagtc ttcacaagtg ttttgtgcga gtagaaaacg ttaaaggggc agtatggaca 540 gtggatgaag tagaatteea aaaacgaagg ceacaaaaga teagtggtaa eeetteeett 600 attaaaaaca tgcagagcag ccacgcctac tgcacacctc tcaatgcagc tttacaggct 660 tcaatggctg agaatagtat acctctatac actaccgctt ccatgggaaa tcccactctg 720 ggcaacttag ccagcgcaat acgggaagag ctgaacgggg caatggagca taccaacagc 780 aacgagagtg acagcagtcc aggcagatct cctatgcaag ccgtgcatcc tgtacacgtc 840 aaagaagagc ccctcgatcc agaggaagct gaagggcccc tgtccttagt gacaacagcc 900 aaccacagtc cagattttga ccatgacaga gattacgaag atgaaccagt aaacgaggac 960 atggagtgac tatcggggcg ggccaacccc gagaatgaag attggaaaaa aaaaa

- (2) INFORMATION ON SEQ ID NO. 96:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2532 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 - ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

gctcgatgtg	caagtgaagg	atgattccag	ggccctgact	ttaggagcac	tgacgctgcc 60)
tctggcccgc	ctgctgactg	ccccagaact	catcctggac	cagtggttcc	agctcagcag 120)
ctctggtcca	aactccagac	tctatatgaa	actagtcatg	aggatcctgt	acttggattc 180)
atcagaaata	tgcttcccca	cggtgcctgg	ttgtcctggt	gcttgggacg	tggacagtga 240	,
gaatccccag	agaggcagca	gtgtggatgc	cccacctcga	ccctgtcaca	cgactcctga 300	į
tagccagttt	gggactgagc	atgtgcttcg	gatccatgta	ttagaggccc	aggacctgat 360	ļ
tgccaaagac	cgtttcttgg	ggggactggt	gaagggcaag	tcagacccct	atgtcaaact 420	,
aaagttggca	ggacgaagct	tccggagcca	tgttgttcgg	gaagatctca	atcccccctg 480	
gaatgaggtt	tttgaggtga	tcgtcacatc	agttccaggc	caagagctag	aggttgaagt 540	
ctttgacaag	gacttggaca	aggatgattt	tctgggcagg	tgtaaagtgc	gtctcaccac 600	
agtettaaac	agtggcttcc	ttgatgagtg	gctgaccctg	gaggatgtcc	catctggccg 660	
cctgcacttg	cgcctggagc	gtctcacccc	ccgtcccact	gctgctgagt	tagaggaggt 720	
gctgcaggtg	aatagtttga	tccagactca	gaagagtgcg	gagctggctg	caaccetact 780	
atccatctat	atggagcggg	cagaggacct	cccgctgcga	aaaggcacca	agcacctcag 840	
cccttatgct	actctcactg	tgggagatag	ttctcataaa	accaagacta	tttcgcaaac 900	
ttcagcccct	gtctgggatg	agagtgcctc	ctttctcatc	aggaaaccac	acactgagag 960	
cctagagttg	caggttcggg	gtgagggcac	tggcgtgctg	ggctcattat	ccctgcccct1020	
ctcagagctc	ctcgtggctg	accagctctg	cttggaccgc	tggtttacac	tcagcagtgg1080	
tcaggggcag	gtgctactga	gagcacagct	agggatcctg	gtgtcccagc	actcgggagt1140	
ggaagctcat	agccacagct	acagccacag	ctcctcatcg	ctgagtgaag	aaccagagct1200	
ctcgggggga	ccccctcaca	tcacctcctc	agccccagag	ctccggcagc	gcctaacaca1260	
tgttgacagt	ccccttgagg	ctccagccgg	gcctctgggc	caggtgaaac	tgactctgtg1320	
gtactacagt	gaagaacgaa	agctggtcag	cattgttcat	ggttgccggt	cccttcgaca1380	
gaatggacgt	gatcctcctg	atccctatgt	gtcactgttg	ctactgccag	acaagaaccg1440	
aggcaccaag	aggaggacct	cacagaagaa	gaggaccctg	agtcctgaat	ttaatgaacg1500	
gtttgagtgg	gaactccccc	tggatgaggc	ccagagacga	aagctggatg	tctctctcaa1560	
gtctaattcc	tectteatgt	caagagagcg	tgactgctgg	ggaaggtgca	gctggaccta1620	
gctgagacag	acctttccca	gggtgtagcc	cggtggtatg	acctgatgga	caacaaggac1680	
aagggcagct	cctaggagct	ggcgagtccc	agcctgactg	ctctgtcttc	ctgccttcgt1740	
ctcgctccat	caccgcctca	atgtgatgag	cctaaagcta	gggtccaagg	gcagagcctg1800	
tgcccttcag	ccctttcacc	taacaggccc	atattcgggc	ctttqcctqa	ccaaagagaa1860	
gaaccgtatg	ttccctttac	tgcacggcct	ttatccttct	gggcccctaa	ggcggggacc1920	
tgagctggct	gtttcctgct	ttgcctgcac	attgttctcc	cttcctccca	actcctcagg1980	
gccttctgta	tctgtgcctg	gccagtggca	gcactagcag	tggtattagc	ttatgccaaa2040	
tacagetttg	gaaggatctt	tttttcttta	actagatggt	caccttcttc	cctaccacac2100	
atgggtggga	aggtggacag	gctaacctct	ccagctgtga	gcctcttaga	ctactgcatg2160	
tagcaaatgt	tcagcagctc	aggcccccat	gtccagttct	gtccccactg	tcctcaaccc2220	
tgtcctgaaa	attctactgc	tttgatggct	ggggccagtc	tcttgtcact	ttggaaactg2280	
aggacgcgtg	gattctactc	aagcctccaa	gtagtggcat	atcagtcttg	gagctcctag2340	
ctggtgatac	ggagagggct	ttggaggact	tgggacagca	gggccaattt	ttttgcccaa2400	
gtgcctaggc	tgctaactca	ctgactagaa	cttaatctgg	tactttacag	ttttgcacca2460	
actctgccaa	gccactggat	cttacattaa	acatcatact	caaaaaaaa	aaaaataaaa2520	
ataaaaaaaa	aa				2532	
					2002	



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 776 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO.
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

tttttttt tttttttt tttttttt tttttgagaca aagteteact gtgteaceca 60 gactggaatg cagtgacaca ateteggete actgaaacet ctgcetteca ggtteaaget120 atteteatge ctcageetet caagtagetg ggactacaga tgtgggecae catgtetggc180 taatttttt tttttttgt agagacaggg tttegecatg ttgaegagae tggtetegaa240 ctcetggeet caagtgatet geegeeteag etteteaaag taetgggatt atataggcat300 gagecactga geetggeet gaagegttt teteaaagge eetetgggat ataaattaga360 tttggcatet eetgteetgg geeagggate tetetacaag ageeeetgee eetetgtgg420 aggeacagtt ttagaataag gaggaggagg gagaagagaa aatgtaaagg agggagatet480 tteecaggee geaceattte tgteacteae atggaeceaa gataaaagaa tggecaaace540 etcacaacee etgatgttg aagagtteea aggtgaaggg gagaaggg aaacaaagaa gtgtttgatg600 gtgecagaga ggggetgete teecagaaage taaaatttaa tttettttt eetetgagt1660 etgtaettea accageetae aagetggeae ttgetaacaa ateagaaata tgacaattaa720 tgattaaaga etgtgattge caccaaaaaa aaaaaaaaa geeaggaaaa aaaggg 776

- (2) INFORMATION ON SEQ ID NO. 99:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 629 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ccaaaatgc tcggcgaaaa cttgctctaa aaaccattga ctgggtagct tttgcagaga120 tcataccca gaaccaaaag gccattgcta gttccctgaa atcctggaat gagaccctca180 cctccaggtt ggctgcttta cctggaatc caccagctat cgactgggct tactacaagg240 ccaatgtggc caaggctgc ttggtggatg actttgagaa gaagtttaat gcgctgaagg300 ttcccgtgcc agaggataaa tatactgccc aggtggatgc cgaagaaaaa gaagatgga360 tctcccaga aaccttgtgc tccctcaa atccattg accaggat tgtagaatat gagaaagga420 cttcccaga aaccaaatta gacaagaaaa agtatcccta ttggcctcac caaccaattg540 agaatttata aaattgagtc caggaggaag ctctggccct tgtattacac catcggaca600 ttaaaaaataa taattaaca aaaaaaaaa 6629

- (2) INFORMATION ON SEQ ID NO. 100:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 757 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

ggcggggagc agggggacac cagggtgaat caggaagacc cgaggggtgg cccccaccct 60 ttctccaccc acgcggcagg ttccaggtgc cctggctgga gtcagtcctc atcgtagtcal20 gcaacaacat tgacgaggag gcgctggccc gactggccca ggagggcagt gaggtgaatg180 tcattggcat tggcaccagt gtggtcacct gccccaaca gccttccctg ggtggcgtct240 ataagctggt ggccgtgggg ggccagccac gaatgaagct gaccgaggac cccgagaagc300 agacgttgcc tgggagcaag gctgctttcc ggctcctggg ctctgacggg tctccactca360 tggacatgct gacgagcag tgccaccag tgggcaggag ctgagggtgt420 ggcctccagg ggcccaggag ccctgcaccg tgaggccagc ccaggtggag ccactactgc480 ggctctgcct ccagcagga cagctgtgt agccgctcc atccctgga cagctgtgta gccgactca gcctgagac cagctgtgta cagcagtacc caggaggcct cagagacctg600 cacagtacca ggtggtgctg tccgagaggc tgcaggccct ggtgaacagt ctgtgtggggccccaagga

- (2) INFORMATION ON SEQ ID NO. 101:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1262 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

aatttgttga agagtgattc tccctcatcc tctgcaaaca ttccataggc gataggaaga actatgeete tgecaagett tetgagttge tgecagaaga agttgaagea gaagtgaaag 120 caqctqcaga gatatcaatg ggaacagagg tttcagaaga agatatttgc aatattctgc 180 atctttgcac ccaggtgatt gaaatctctg aatatcgaac ccagctctat gaatatctac 240 aaaatcqaat qatqqccatt qcacccaatg ttacagtcat ggttggggaa ttagttggag 300 cacqqcttat tgctcatgca ggttctcttt taaatttggc caagcatgca gcttctaccg 360 ttcaqattct tggagctgaa aaggcacttt tcagagccct caaatctaga cgggataccc 420 ctaaqtatqq totcatttat catgottcac togtqqqoca qacaaqtooc aaacacaaaq 480 gaaagatttc tcgaatgctg gcagccaaaa ccgttttggc tatccgttat gatgcttttg 540 qtqaqqattc aagttctgca atgggagttg agaacagagc caaattagag gccaggttga 600 gaactttgga agacagaggg ataagaaaaa taagtggaac aggaaaagca ttagcaaaaa 660 cagaaaaata tgaacacaaa agtgaagtga agacttacga teettetggt gacteeacae 720 ttccaacctg ttctaaaaaa cgcaaaatag aacaggtaga taaagaggat gaaattactg 780 aaaagaaagc caaaaaagcc aagattaaag ttaaagttga agaagaggaa gaagaaaaag 840 tggcagaaga agaagaaaca tctgtgaaga agaagaagaa aaggggtaaa aagaaacaca 900 ttaaggaaga accactttct gaggaagaac catgtaccag cacagcaatt gctagtccag 960 agaaaaagaa gaaaaagaaa aaaaagagag agaacgagga ttaacagaaa ggaattacga1020 ttatatcacc cggacacaca tcatgcttaa gattcaactg ggagcatacc agggatgctc1080 tctaacgtaa tcaagggaag gttcagtaag acaaagtgat ttatcatcta taacttcaaal140 cctatttgtc ttgacatcaa ctctgttaac cttatgtcat catttcttag agtctttgat1200 1262

(2) INFORMATION ON SEQ ID NO. 102:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1281 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

qqcqqaaqta gccgcaggca tggcggcggc tatgccgctg ttgctctgct cgtcctgttg ctcctggggc ccggcggctg gtgccttgca gaacccccac gcgacagcct gcgggaggaa 120 cttgtcatca ccccgctgcc ttccggggac gtagccgcca cattccagtt ccgcacgcgc 180 tgggattcgg agcttcagcg ggaaggagtg tcccattaca ggctctttcc caaagccctg 240 gggcagctga tctccaagta ttctctacgg gagctgcacc tgtcattcac acaaggcttt 300 tggaggaccc gatactgggg gccacccttc ctgcaggccc catcaggtgc agagctgtgg 360 gtctggttcc aagacactgt cactgatgtg gataaatctt ggaaggagct cagtaatgtc 420 ctctcaggga tcttctgcgc ctctctcaac ttcatcgact ccaccaacac agtcactccc 480 actgeetect teaaacceet gggtetggee aatgacactg accaetactt tetgegetat 540 gctgtgctgc cgcgggaggt ggtctgcacc gaaaacctca ccccctggaa gaagctcttg 600 ccctgtagtt ccaaggcagg cctctctgtg ctgctgaagg cagatcgctt gttccacacc 660 agctaccact cccaggcagt gcatatccgc cctgtttgca gaaatgcacg ctgtactagc 720 atctcctggg agctgaggca gaccctgtca gttgtatttg atgccttcat cacggggcag 780 ggaaagaaag actggtccct cttccggatg ttctcccgaa ccctcacgga gccctgcccc 840 ctggcttcag agagccgagt ctatgtggac atcaccacct acaaccagga caacgagaca 900 ttagaggtgc acccacccc gaccactaca tatcaggacg tcatcctagg cactcggaag 960 acctatgcca totatgactt gottgacacc gocatgatca acaactotcg aaacctcaac1020 atccagetea agtggaagag acceeeagag aatgaggeee ecceagtgee etteetgeat1080 gcccagcggt acgtgagtgg ctatgggctg cagaaggggg agctgagcac actgctgtac1140 aacacccacc cataccgggc cttcccggtg ctgctgctgg acaccgtacc ctggtatctg1200 cggctgttac atccactacc agcctgccca ggaccggctg caaccccacc tcctggagat1260 gctgattcag ctgccggcca a

- (2) INFORMATION ON SEQ ID NO. 103:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 716 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```
gggccccaga aagagaccaa tgtgttgtgc gacgggtggg tggcagtggc agtggcagat 60 ggtaccaggc gccccagaac tctaaggggc ctcaagtagt ttaaaacctc ggaggctgcc120 tgacttgggg ccaagggtt ctatgctcag gcctgacccc tcatggatta gtttctgctg180 gaaaaacttt ttctgccctc ggccaggtct ctatctcctt ctgccttaac atattttgga240 aggttggttc ccagcagaga cggggccatg ggctcacact ctgacctctc ccaccggcatt300 agccctgtct cagcctctgg gctgttacgc aagttaattc ctgcacaaga ctcacaacag360 ggctgtggag gaagcaaagg agcccttttt atgcctctgt agtaggactg agaggaggccc420 tctggccagc gtgagcctgc tggttcttcc cggactgtac caggccttga ggcggggtat480 ggaaacgccc cactctgggg cctggcttgg ggaagggag gcggcagggg ttctttgggc540 ttctcgaggg tataatctga gctctctgg gaacgtgtg ccatttgtag gcagtagtcc600 gacacgtcgg gggactcaac tttacactgg gacaatctgt gtgtggtctg ttttgtagaa660 attcatcac acaagagagt ggaggcatga acaggggtgg ccttcctcgg atctc
```

(2) INFORMATION ON SEQ ID NO. 104:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1160 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```
tttgttgttg gagaaaggag agaaaggaaa gcgcgagggg ccgccgccac caccagcgca
gagteetgga getgtgagga gattegggee gteaceetge eteceetgeg tecegeeace 120
ggccgcttct gtcctcggac ccattccaac aatctcgtaa aacatggtgg attactatga 180
agttctaggc gtgcagagac atgcctcacc cgaggatatt aaaaaggcat atcggaaact 240
ggcactgaag tggcatccag ataaaaatcc tgagaataaa gaagaagcag agagaaaatt 300
caagcaagta geggaggeat atgaagtget gteggatget aagaaaeggg acatetatga 360
caaatatggc aaagaaggat taaatggtgg aggaggaggt ggaagtcatt ttgacagtcc 420
atttgaattt ggcttcacat tccgtaaccc agatgatgtc ttcagggaat tttttggtgg 480
aagggaccca ttttcatttg acttctttga agaccctttt gaggacttct ttgggaatcg 540
aaggggtccc cgaggaagca gaagccgagg gacggggtcg tttttctctg cgttcagtgg 600
atttccgtct tttggaagtg gattttcttc ttttgataca ggatttactt catttgggtc 660
actaggicae gggggeetea etteattete tiecaegtea titiggtggta gtggeatggg 720
caacttcaaa tcgatatcaa cttcaactaa aatggttaat ggcagaaaaa tcactacaaa 780
gagaattgtc gagaacggtc aagaaagagt agaagttgaa gaagatggcc agttaaagtc 840
cttaacaata aatggtgtgg ccgacgacga tgccctcgct gaggagcgca tgcggagagg 900
ccagaacgee etgecageee ageetgeegg ceteegeeeg eegaageege eeeggeetge 960
ctegetgetg agacaegege eteactgtet etetgaggag gagggegage aggaeegaee1020
tggggcaccc gggccctggg accccctcgg cgtccgcagc aggattgaaa gaaggtggcal080
agaggaagaa gcagaagcag agagaggagt ttgaaggagg aaggaagttg gaccaaaggc1140
attgattaga ccggattttt
                                                                  1160
```

- (2) INFORMATION ON SEQ ID NO. 105:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1040 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

agcatccgct tccggttccc agactgaatt gtcagtgagc ggagtctgag gtcgctgtgg actgcccact gggccttgcc cgagatggac agccggattc cttatgatga ctacccggtg 120 gttttcttgc ctgcctatga gaatcctcca gcatggattc ctcctcatga gagggtacac 180 cacceggact acaacaatga gttgacceag tttctgcccc gaaccatcac actgaagaag 240 cctcctggag ctcagttggg atttaacatc cgaggaggaa aggcctccca gctaggcatc 300 ttcatctcca aggtgattcc tgactctgat gcacatagag caggactgca ggaaggggac 360 caagttctag ctgtgaatga tgtggatttc caagatattg agcacagcaa gqctqttqaq 420 atcctgaaga cagctcgtga aatcagcatg cgtgtgcgct tctttcccta caattatcat 480 coccaaaaag agaggactgt gcactagaaa gttgcagccc acagcccttc atgtggactc 540 tgtcatgaca tgctaactag acttcagggg agccacttct gttttcagcc cctccctgga 600 atagtgagtt gggaggatgg ggagacagct aaccaactgc attacccaaa ccatattgca 660 cttttagttc cctagttttc taggtgagct tcattccctg aaaggaggat gatgatatct 720 aggcataacc tagcctgtga ggaacctagt taggaaagac aactgacatt tattgaatat 780 catgcactag tecettacat atgteatatt ttaattatag aaateagtag caaaaagaat 840 cttggggatt ttccatctga cttccctggc catcttatcc catccttgca ctaccagaag 900 atteatacae ttttgagaet ceagtgagae getgttttea eceetteete eteetageet 960 gggccggccg gtgggtggtc 1040

- (2) INFORMATION ON SEQ ID NO. 106:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1336 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```
cgagggacag aacctggtgc aggaggagtt ggcggcccgc gggacccagc ccccgtccat
ccgcaacggc ctggacaaag ccgcgaggtc cgcttcgagc gagctgagca ggccctgcgc 120
eggttcagec agggccccac accegetgee getgtccccg agggcacggc agecgagggc 180
gctcccaggc aggaaaactg tggtgcccag caggtccccg caggccgggc actagcaccc 240
ctcccagcag ccccgtgcgg acctgcgggc ccctgacgga tgaggacgtg gtcaggctgc 300
ggccctgtga gaagaagcgg ctggacatcc gtggcaaact ttacctggcc cccctcacca 360
cgtgtgggaa cctgcccttc cgacggatct gcaagcgctt cggggcggat gtgacatgtg 420
gagagatggc cgtctgcacc aacctgctgc agggccagat gtccgagtgg gccctactca 480
aacgccacca gtgtgaggac atctttggcg tccagctgga gggcgccttc cccgacacca 540
tgaccaagtg tgccgagctg ctgagccgca ccgtggaggt ggactttgtg gacatcaacg 600
teggetgeee categacete gtgtacaaga agggtggggg etgtgeeete atgaateget 660
ccaccaagtt ccagcagatc gtccgtggca tgaaccaggt gctggatgtg ccgctqactg 720
tgaagatccg cacaggcgtc caggagcgtg tgaacctggc gcaccgcctg ctgcccqagc 780
tgcgggactg gggcgtggca ctcgtcacgg aaatggggac atcttgtcat ttgaggatgc 840
caaccgcgcc atgcagactg gtgtcaccgg gatcatgatt gcccgtggcg ccctqctcaa 900
gccgtggctc ttcacggaga tcaaggagca gcggcactgg gacatctcgt cgtccgagcg 960
cctggacatc ctgcgggact tcaccaacta cggcctggag cactggggct cggacacgca1020
gggcgtggag aagacccggc gctttctgct cgagtggctg tccttcctgt gccggtacga1080
toccgtgggg ctgctggagc ggctcccaca gaggatcaac gagcggccgc cctactacct1140
gggccgcgac tacctggaga cgctgatggc cagccagaag gcagccgact ggatccgcat1200
cagegagatg etecttggge cagtgeece caectegeet tettgeegaa geacaaggee1260
aacgcgtaca agtagcctca ggctttccca ggggcaccct ggggcgagga gagtacaata1320
aattttattc ttttaa
```

- (2) INFORMATION ON SEQ ID NO. 107:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 812 base pairs
 - (B) TYPE: Nucleic acid

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

- (2) INFORMATION ON SEQ ID NO. 108:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2681 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN: (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```
qatqcttqqt atcatcatca tgatqacqct qtqtqaccaq qtqqatattt atqaqtqcct 60
cccatccaag cgcaagactg acgtgtgcta ctactaccag aagttcttcg atagtgcctg 120
cacqatqqqt qcctaccacc cqctqctcta tqaqaaqaat ttqqtqaaqc atctcaacca 180
qqqcacaqat qaqqacatct acctqcttqq aaaaqccaca ctqcctqqct tccqqaccat 240
tcactgctaa gcacaggctc ctcactcttc tccatcaggc attaaatgaa tggtctcttg 300
gecaceccag cetgggaaga acatttteet gaacaattee ageetgetee tittaeteta 360
ggggcctctg tcagcaagac catggggact tcaagagcct gtggtcagga aatcaggtcc 420
agcettecet gtagecagae agtttatgag eccagageet ectgecaeae acatgeaeae 480
atatctagca ttctttccag acagcatcct ccccgccttc caccttggta gatgcaaggt 540
ctatctctcc catcagggct gccaaagctg ggctttgttt ttcccagcag aatgatgcca 600
ttctcacaaa ccaatgctct atattgcttg aagtctgcat ctaaatattg atttcacgtt 660
ttaaagaaat totottaaat tacaattgtg cocaatgcag ggtggctotg gggggcaagt 720
aggtggtaca ggggattgga aacatgctcc gcgcctccag agaaaagttg ctcccqaggt 780
ccatgcccct ggaacgtgtt cctatcactc tggctggttg ggctggtcct tagactgggt 840
gettatgatt aaagggtett ggttageeca ettteeetet eeatgtggag atggaaggta 900
gagaaggata cagtgtctat cctcaagttg ctacggttca gtgagagagg cagacatctg 960
aacaggcagg taggattcag tgtgctcagt gcactgggga tttggagaga gatgggcttg1020
ctctctctgt gcacccagga gggccacgca cttaaaactg tgtttgtgga tcagagaagg1080
ctttatagca cagggggcat tcagatgagt cttagaggaa gagaagaaac atggcaagcal140
gattacatct gagccgtttg aattgtgttt ttctttcttc ccatgtttat tttctaagat1200
ctacctgaac ttagagactc aagatatttt tttaggaaac ctcctaccca tgtctgaggt1260
agcaagtgca gcctcacgac agataccagg caatccagag ccacaaaacg tgattcctcc1320
aggetetgee tggeetgace etgteetgte agetgggttt acataceagt eccattette1380
cttttcaata aataccccca aatcttctcc taaccaccat taaagcattt tttgctttaa1440
aagcatectg acceeaattt etttgagete aegggeettt tgetgaaggt eteteagggt1500
gtagtggtgt ggctctctgg acttaacgtc actctcagag gtcagaacct tggagatcag1560
aactgattct caccaggtgt gagaggtgtg gtagcagatt gcaatgctct gcacctcttc1620
cttgcaagtg agcaacttca ggctctctgg gcagaggctg gcccactgta gtttgcagac1680
atgctctcca gatggtttta ctaagtcccc tctccctgat agggaatcct gctggaccag1740
cgcagcctgg gtgtggagag gttaaaagac ttgcacagga tcaccaagtc atgctgtaga1800
gccaggattc ctagacccag ggctctgcac tctcaaggct ggccccatgt gctcaagggg1860
atctaatgtt tgggctccaa actaaccatc tcggagctgg gctcctcatt tactgccaaa1920
ccctcagctt atgtagctag aaagggccct ggagtgagaa agcctggatt ttcaaattga1980
tgctccccta ctgactagct gtgccactct gggcaaatgc tcttccttga gcctgtttcc2040
acacctgtaa agtggggatg atgatcctat ctcactgctt ttgtgaggat tacaggaaag2100
cacctgtcct ggctctgtac ctggcacgta gtaggtgctc agttcatgct ggtttccttc2160
ctgcctttag tagggacctg ctctgtgctc acacctcggc tgcatgcacc ctgctgtgac2220
ggaggctagt gtggaagagg teetgteete agggaattaa etgtettatt gggagaeaac2280
aactgtcctc cttggaacac ccaagaaacc atgcaaagca gtggacaaca cagaacacgc2340
cctcctcctc gctgcctgca gctccaatct gattctgctt gggaatgggc ggagcacgtg2400
ggctgcttaa ctgctgtata ggacaagccc cttacccctc tctgggccca tgaattcctg2460
gcttggttta tgttctgatt tgacacactg attttaatct tcgaatcatg acactgagtg2520
cagaggaggt ggcattccga cagcaggaca tacatgttgg tgtgaagact gggacgacac2580
tgggtagaat ctagttttta attattatta atataaagga tcaaattaat ttaaatatga2640
atccgaagtc cacagaactt taagtgctgt gccggccatg t
                                                                 2681
```

(2) INFORMATION ON SEQ ID NO. 109:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1407 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```
cttgggacgg aagcctagct gggtgggggg cgccgggctg gagccttcgc aggggagcgg
getcagteat caccetgege eccagagtga etcageecce aegtececae ceatecegg 120
ggagccaggg ccgcagaggg aggtagataa gtggggtggc agcctgggtc ggccagagag 180
ttcaggccac cccggccgga cgcctgccac ttgctgtcac tgtgccgctg tcatggcacg 240
ctccgggagt gccacgccac ctgcccgggc tccgggagcc cctccacgga gcccacccca 300
gaggetggta caggatgtca gtgggecect gagggagetg egecetegge tetgecacet 360
gcgaaaggga cctcagggct atgggttcaa cctgcatagt gacaagtccc ggcccggcca 420
gtacatecge tetgtggace egggeteace tgeegeeege tetggeetee gegeeeagga 480
ccggctcatt gaggtgaacg ggcagaatgt ggagggactg cgccatgctg aggtggtggc 540
caqcatcaag gcacgggagg acgaggcccg gctgctggtc gtggaccccg agacagatga 600
acacttcaag cggcttcggg tcacacccac cgaggagcac gtggaaggtc ctctgccgtc 660
accogtcace aatggaacea geeetgeeea geteaatggt ggetetgegt getegteeeg 720
aagtgacctg cctggttccg acaaggacac tgaggatggc agtgcctgga agcaagatcc 780
cttccaggag agoggoctcc acctgagocc cacggoggoc gaggocaagg agaaggotog 840
agccatgcga gtcaacaagc gcgcgccaca gatggactgg aacaggaagc gtgaaatctt 900
carcaactte trageceett cetreette terggaceet graceette eegeacrage 960
cttgggcctc agcctgcccc gagctccccc agcctcagtg gactggaggg tggtcctgcc1020
attgcccaga aatcagcccc agccccggtg agcccccatc ctgcccctgc ccaccaggta1080
ctgggggcct gtggcagcaa gataggggga gagagaccca gagatgtgag agagagtcag1140
eqeqeqqeag cegeggggeg agggeetttg etgetetgee ggggeetget gaetgaaagg1260
aatttgtgtt tttgcttttt ttccaaaaag atctccagct ccacacatgt ttccacttaa1320
taccagagac coccoccgto aaagcccccc tocccggccc cttgggacgc gctctaaata1380
attgcaataa aacaaacctt tctctgc
                                                               1407
```

(2) INFORMATION ON SEQ ID NO. 110:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1376 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```
cgaagaagcc ccgccccgtc ccgcttagac aatgccccgg agccgccaga ccgtcgcgcc 60
cctgccccat cgtagtatat gagctcgcct acacaaggac ccccgctaaa agccagagct 120
cccagtcccc gaggettgaa gacggggact cccttctcca ccaactctgt cctcgggggg 180
tggggcccca gccgagatca cagcgcgaca ggagtggggg tggccgctgg agacaggtga 240
ggacgccggg ggaggggctg ggccgctgct cccatgccct gatccgggga gtcccaqaqa 360
geotggegte gggggaaggt gegggggetg geetteeege tetggatetg gecaaagete 420
aaagggagca cggggtgctg ggaggtaaac tgaggcaacg actggggcta cagctgctag 480
aactgccacc tgaggagtca ttgccgctgg gaccgctgct tggcgacacg gccqtqatcc 540
aaggggacac ggccctaatc acgcggccct ggagccccgc tcgtaggcca gaggtcgatg 600
gagtccgcaa agccctgcaa gacctggggc tccgaattgt ggaaatagga gacgagaacg 660
cgacgctgga tggcactgac gttctcttca ccggccggga gtttttcgta ggcctctcca 720
aatggaccaa tcaccgagga gctgagatcg tggcggacac gttccgggac ttcgccgtct 780
ccactgtgcc agtctcgggt ccctcccacc tgcgcggtct ctgcggcatg gggggacctc 840.
gcactgttgt ggcaggcagc agcgacgctg cccaaaaggc tgtccgggca atggcagtgc 900
tgacagatca eccatatgee teeetgacee teecagatga egeagetget gaetgtetet 960
ttottogtoc tgggttgcct ggtgtgcccc ctttcctcct gcaccgtgga ggtggggatc1020
tgcccaacag ccaggaggca ctgcagaagc tctctgatgt caccctggta cctgtgtcct1080
gctcagaact ggagaaggct ggcgccgggc tcagctccct ctgcttggtg ctcagcacac1140
gcccccacag ctgagggcct ggccttgggg tactgctggc caggggtagg atagtatagg1200
aagtagaagg ggaaggaggg ttagatagag aatgctgaat aggcagtagt tgggagagag1260
cctcaatatt gggggaggg agagtgtagg gaaaaggatc cactgggtga atcctcctc1320
```

- (2) INFORMATION ON SEQ ID NO. 111:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 854 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

- (2) INFORMATION ON SEQ ID NO. 112:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1681 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```
ttcagctttt gccgaaatgg gtagtgatca cacacagtca tctgcaagca aaatctcaca 60
agatgtggac aaagaggatg agtttggtta cagctggaaa aatatcagag agcgttatgg 120
aaccctaaca ggcgagctgc atatgattga actggagaaa ggtcatagtg gtttgggcct 180
aagtettget gggaacaaag accgatccag gatgagtgte tteatagtgg ggattgatee 240
aaatggagct gcaggaaaag atggtcgatt gcaaattgca gatgagcttc taqagatcaa 300
tggtcagatt ttatatggaa gaagtcatca gaatgcctca tcaatcatta aatgtgcccc 360
ttctaaagtg aaaataattt ttatcagaaa taaagatgca gtgaatcaga tggccgtatg 420
tcctggaaat gcagtagaac ctttgccttc taactcagaa aatcttcaaa ataaggagac 480
agagccaact gttactactt ctgatgcagc tgtggacctc agttcattta aaaatgtgca 540
acattetgga getteecaag gaggeagggg ggtttgggta ttgetateag egaagaagat 600
acactcagtg gagtcatcat aaagagctta acagagcatg gggtagcagc cacggatgga 660
cgactcaaag tcggagatca gatactggct gtagatgatg aaattgttgt tggttaccct 720
attgaaaagt ttattagcct tctgaagaca gcaaagatga cagtaaaact taccatccat 780
gctgagaatc cagattccca ggctgttcct tcagcagctg gtgcagccag tggagaaaaa 840
aagaacagct cccagtctct gatggtccca cagtctggct ccccagaacc ggagtccatc 900
cgaaatacaa gcagatcatc aacaccagca atttttgctt ctgatcctgc aacctgcccc 960
attatecetg getgegaaac aaccategag atttecaaag ggegaacagg getgggeetg1020
agcatcgttg ggggttcaga cacgctgctg ggtgccatta ttatccatga agtttatgaa1080
gaaggagcag catgtaaaga tggaagactc tgggctggag atcagatctt agaggtgaat1140
ggaattgact tgagaaaggc cacacatgat gaagcaatca atgtcctgag acagacgcca1200
cagagagtgc gcctgacact ctacagagat gaggccccat acaaagagga ggaagtgtgt1260
gacaccctca ctattgagct gcagaagaag ccgggaaaag gcctaggatt aagtattgtt1320
ggtaaaagaa acgatactgg agtatttgtg tcagacattg tcaaaggagg aattgcagat1380
gccgatggaa gactgatgca gggagaccag atattaatgg tgaatgggga agacgttcgt1440
aatgccaccc aagaagcggt tgccgtttgg ataaaagtgt ttccctaggg cacagttaac1500
cttgggaagt tgggaaggat tcaaagctgg gtcccgttcc gtttcaggag gagggagggc1560
cgtttttcaa aggcagccca gggttgagtt tgaaggggca gcctctttcg tcttttttca1620
cgtttttccc acttttttgg ggatccccgt ttacattttg agttccactt ggggaagtta1680
```

(2) INFORMATION ON SEQ ID NO. 113:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 852 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ggcaatttcc gttaggtgct gaaggctgtg gcgcggct gtcccattc ccacgtgaag 60 cgctacgcta gcatcgctcg gctggcggct cccagctcgc cgcggagcag tcccggcagc120 agcgggggac cggaagtggc tcgcggagc tcagaagcta gtcccggagc ccggcgtgtg180 gcgcctcgga gcacggtgac ggcgccatgt ccctaatctg ctccatctct aacgaagtgc240 cggagcaccc atgtgtatcc cctgtctcta atcatgtta tgagcggggg ctcatcgaga300 agtacattgc ggagaatggt accgaccca tcaacaacca gcctctctcc gaggagcagc360 tcatcgacat caaagttgct caccaatcc ggcccaagcc tccctcagcc accagcatcc420 cggccatct gaaagctttg caggatgagt gggatgcagt catgctgcac agcttcactc480 cgcccaagag ctgcagaaa cccgccaaga gctgtcacac gctctgtacc agcacgatgc540 cgcctgccgt gtcattgccc gtctcaccaa ggaaactgtg aaggggatgg gcaggagggc600 ttgtgcaggg ttttgtaagc agtgatctag tttcattaaa aaaagaaaac aataaaaaag660 ccctgcacaa ggcctacaac ccctctccct tcctgtcgtc caatggacgt ggtggtggct720 gttccacacc cattttgttg cagttcctgt gagacaggag aggctgagc aggctgagcc aggtgtcatca840 aaaaaaaagaga ac ggcgaggagg ggttttgtaa gcagtgatct agttcatta840 aaaaaaaagaga

(2) INFORMATION ON SEQ ID NO. 114:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1739 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```
ttcacggatg cggacgacgt agccatcctt acctacgtga aggaaaatgc ccgctcgccc 120
ageteegtea eeggtaaege ettgtggaaa gegatggaga agageteget eaegeageae 180
tegtggeagt ecetgaagga eegetacete aageaeetge ggggeeagga geataagtae 240
ctgctggggg acgcgccggt gagcccctcc tcccagaagc tcaagcggaa ggcggaggag 300
gaccoggagg cogoggatag oggggaacca cagaataaga gaactocaga tttgcctgaa 360
gaagagtatg tgaaggaaga aatccaggag aatgaagaag cagtcaaaaa gatgcttgtg 420
gaagccaccc gggagtttga ggaggttgtg gtggatgaga gccctcctga ttttgaaata 480
catataacta tgtgtgatga tgatccaccc acacctgagg aagactcaga aacacagcct 540
gatgaggagg aagaagaaga agaagaaaaa gtttctcaac cagaggtggg agctgccatt 600
aagatcattc ggcagttaat ggagaagttt aacttggatc tatcaacagt tacacaggcc 660
ttcctaaaaa atagtggtga gctggaggct acttccgcct tcttagcgtc tggtcagaga 720
gctgatggat atcccatttg gtcccgacaa gatgacatag atttgcaaaa agatgatgag 780
gataccagag aggcattggt caaaaaattt ggtgctcaga atgtagctcg gaggattgaa 840
gttaaaaaaa attgtgacca atgaacttta gagagttctt gcattggaac tggcacttat 960
tttctgacca tcgctgctgt tgctctgtga gtcctagatt tttgtagcca agcagagttg1020
tagaggggga taaaaagaaa agaaattgga tgtatttaca gctgtccttg aacaagtatc1080
aatgtgttta tgaaaggaag atctaaatca gacaggagtt ggtctacata gtagtaatcc1140
attgttggaa tggaaccctt gctatagtag tgacaaagtg aaaggaaatt taggaggcat1200
aggccatttc aggcagcata agtaatctcc tgtcctttgg cagaagctcc tttagattgg1260
gatagattcc aaataaagaa tctagaaata ggagaagatt taattatgag gccttgaaca1320
eggattatee ceaaaceett gteattteee ceagtgaget etgattteta gaetgetttg1380
aaaatgctgt attcattttg ctaacttagt atttgggtac cctgctcttt ggctgttctt1440
tttttggage cetteteagt caagtetgee ggatgtettt etttacetae eceteagttt1500
teettaaaae gegeacaeaa etetagagag tgttaagaat aatgttaett ggttaatgtg1560
ttatttattg agtattgttt gtgctaagca ttgtgttaga tttaaaaaaat tagtggattg1620
actccacttt gttgtgttgt tttcattgtt gaaaataaat ataactttgt attcgaaaaa1680
aaaaaaaaa aaaaaaaaag gaggagaaaa agaggggaaa gggggaagag gagcaaaga 1739
```

- (2) INFORMATION ON SEQ ID NO. 115:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 805 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

- (2) INFORMATION ON SEQ ID NO. 116:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1483 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```
tgaaaaagac ccaacgccaa cacctggtgc cttttgcagc cagcgcccac ccatccgtgc 60
coggaccett gggaatgeec geggetecag aggaaaaage ccagggacgg ggeetecgtt 120
geggggggte ggetgettet tgggaacttt gtegttteeg gegetggetg getggetgge 180
tgtaaagcac tgaagccccc cggccgccaa cccctgaaag cagaacctgg cctccctggc 240
cacageagee tracecaceg eretaegtgt ecegggeact tecegeagee trecegreee 300
ttteteateg geettgtagt tgtacagtge tgttggtttg aaaaggtgat gtgtggggag 360
tgcggctcat cactgagtag agaggtagaa tttctattta accagacctg tagtagtatt 420
accaatccag ttcaattaag gtgatttttt gtaattatta ttattttggt gggacaatct 480
ttaattttct aaagatagca ctaacatcag ctcattagcc acctgtgcct gtccccgcct 540
tggcccggct ggatgaagcg gcttccccgc agggccccca cttcccagtg gctgcttcct 600
ggggacccag ggcaccccgg caccttcagg cacgctcctc agetggtcac ctcccggctt 660
tgccgttcag atggggctcc tgaggctcag gagtgaagat gccacagagc cgggctcccc 720
taggetgegt egggeatget tggaagetgg eetgeeagga eetteeacce tggggeetgt 780
gtcagccgcc ggccctccgc accctggaag cacacggcct ctgggaagga cagccctgac 840
cttcggtttt ccgagcacgg tgtttcccaa gaattctggg ctggcggcct ggtggcagtg 900
ctggagatga ccccgagccc ctccccgtgg ggcacccagg agggccctgc cggaatgtgc 960
agcctgtggg tagtcggctg gtgtccctgt cgtggagctg gggtgcgtga tctggtgctc1020
gtccacgcag gtgtgtggtg taaacatgta tgtgctgtac agagagacgc gtgtggagag1080
agccgcacac cagcgccacc caggaaaggc ggagcggtta ccagtgtttt gtgtttattt1140
ttaatcaaga cgtttcccct gttttcctat aaatttgctt cgtgtaagca agtacataag1200
gacceteett tggtgaaate egggttegaa tgaatatete aaggeaggag atgeatetat1260
tttaagatge tttggageag acagetttag cegtteecaa teettageaa tgeettaget1320
gggacgcata gctaatactt tagagaggat gacagatcca taaagagagt aaagataaga1380
gaaaatgtct aaagcatctg gaaaggtaaa aaaaaaaaa tctatttttg gacaaatgta1440
attttatccc ccatgggatg cttgggtatg gcgggggga ggc
                                                                 1483
```

- (2) INFORMATION ON SEQ ID NO. 117:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1347 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```
tgaggtcttc catgactgca agtgttatat tggactggat ggtcatgaag tccctttcat
agccagagat tttgtgtggc tgctaaaatg cttacatctc tggctatgaa agggacttca 120
tgaccatcca gtccaatata acacttgcag acagagaaac tgaggtcttc catgacttgc 180
ctagtctccc agctagtttg aggcaaaact ggattcccac tctggtattc tttcttccct 240
ttacatcatt ttccctcctt tataatgtcc tgagagacca gaactcacac cagaatcgat 300
tattcctcag gtgaagcata gactctttca tggtagacag atttcacgac tcagagatag 360
aaatctcttg ctatcatcag gtcacgggca gctcctgtgg agtcctgccc aacttatgtg 420
gcttccataa aatggcaaca gtccaggctc cttgcctaat tttagagcat taactcccta 480
attgccagta agcaaggagg tggatctctg caaacctaca ctgtctatga cagctctagt 540
tqtacttqqt qtqactaaat acctcaaaqq caacctqctt ctqcaqqttt tqaaqtqtca 600
qcttcataaq acactqagqt ttagaattgt ttgattctag accataactg aagggcataa 660
atggaaacag gatatgaagg gaaacaagta gcatcatgga gctgaaaagt ggtgcatcac 720
ccaatggcta gcacaaacaa ggatcacact gtccattctc ttgtctgcta aattaagcat 780
tttcttgcct cctttgcttc atcttttcac aacagctgga tagagggatc agaaatgact 840
gtgtcatggt gctcattcac tgcaaactcc cagttgcaag ctccttggct cccccggagg 900
gagcaagaat ctcatagttc agagacacag agggcctttt agccctaatg accttttgga 960
tgggactgca actcatgact atcctgatat tggaagaaag gactttgtta atcttctccc1020
ccatagetet getgegtagg tetacatett acteagaate actacacatt cetttagtet1080
tectecaage tecagageea tiggiacaaa igettiatig aaactaaata cataatacael140
acaatgagat gaagacaata tagaagtccg catagtcatc ataatcccgt tccttggccg1200
gttgaggcag ctcagtggct gagcccagtc aagccaaccc gcagcttcac tcacgacttc1260
aagatttgat gctaattctt ttggatttct acagttatta aataagtgtc tgagtggaaa1320
aaaaaaaaa aaaaaaaaa aaaaaat
                                                                  1347
```

(2) INFORMATION ON SEQ ID NO. 118:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1683 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```
aatteggeae gatgggggga ateteegaee eegaeaeeet acacatetgg aagaceaaea
                                                                   60
geetteetet eeggttetgg gtgaacatee tgaagaacee eeagtttgte tttgacateg 120
acaagacaga ccacatcgac gcctgccttt cagtcatcgc gcaggccttc atcgacgcct 180
getecatete tgacetgeag etgggeaagg attegeeaac caacaagete etetacgeea 240
aggagattee tgagtacegg aagategtge agegetacta caageagate caggacatga 300
egeogeteag egageaagag atgaatgeee atetggeega ggagtegagg aaataccaga 360
atgagttcaa caccaatgtg gccatggcag agatttataa gtacgccaag aggtatcggc 420
cgcagatcat ggccgcgctg gaggccaacc ccacggcccg gaggacacaa ctgcagcaca 480
agtttgagca ggtggtggct ttgatggagg acaacatcta cgagtgctac agtgaggcct 540
gagacacatg gagagttggt caggctgctg ctgggagaaa tggacgccca ctgggcctca 600
acttgatctt ctaccccgtg cctgtgactc agactgggaa atactgagca gagacggctg 660
gggcgggggc aggaggaggg gctgctctct gagacagggg cgcccccgcc ttgacccctg 720
ggcaccteca tecectecca ectgtececa gateagtete tgggatggag gecagagage 780
tggtcagget eccecatetg eccageaegg ectgeaetgt geceaeceae ttgetceaea 840
acqtccagtt ggtcctgctg ccaagagccc cgtgcatcca ggcggccaag cacaaactgg 900
gggagaggag geogecagee eggaggetge ageccagaaa etetacetea tecacactgg 960
tgcagggagc cctccttgaa ctgacctttg attggtttct gcttcaacta ccaaaatgtt1020
atotocactt cocceteace cgtagaggat cetggecaca gacagtttca agtagtgtca1080
gatttttgtt gcttgggcgg ctgttggtag agtgggcagt gcccgcgcca tggggtgctc1140
tgtgggcttc tccaggagca gggagggtgg aggggaggga tggggggcac aggagctggg1200
agccccgtct ccaggaaaag gagaggggtt aagatgcacc gaggctgtag ctgggctact1260
tgatcttgct gaaagtgttt ctaaagatag caccactttt ttttttaaag cttttatata1320
ttaaaaaacg tatcatgcac caactgtgaa tagctgccgc ttgcgcagag gacccgggga1380 ....
ggggteecga gaggeteece atgeaacaet ggaaatgaet gtteeagaga gegggeagae1440
ctggcagage geceetggeg eetgagacta ceaeceaete egtteetgee agaaacgace1500
ctctgtggcc gatgggccat gcgggccct cgcagccaac tcagccagtg ttgggactgg1560
ctcagagccc atgggggctg gagggggca gctgggactc tggaatcttc tttataataa1620
aagccttacg gacaaaccta aaaaaaaaa aacaagacaa gagagggaaa gggaaagaag1680
ggg
                                                                 1683
```



- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1355 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```
acaagcatgg aagctttact gtttcggctc ttcaaacttc cagcaactac actgcggtgc
atoggactic gacgocoget ggtgacgcac acgotgogoc ggaagtgtga acacaaagco 120
tccaggettt gtcatggegg etgetgetge acgetggaac catgtgtggg teggeacega 180
gactgggatc ttgaaagggg taaatcttca qcgaaaacag gcggcgaact tcacggccgg 240
aggacageeg eggegegagg aggeagtgag egecetgtgt tggggcaeeg geggegagae 300
ccagatgctg gtgggctgcg cggacaggac ggtgaagcac ttcagcaccg aggatggcat 360
attccagggt cagagacact gcccgggcgg ggagggcatg ttccgtggcc tcgcccaggc 420
cgacggcacc ctcatcacat gtgtggattc tgggattctc agagtctggc atgacaagga 480
caaggacaca teetetgace caeteetgga actgagagtg ggeeetgggg tgtgtaggat 540
gegecaagae ecageacaee eccatgtggt tgccacaggt gggaaagaga atgetttgaa 600
gatatgggac ctgcagggct ctgaggaacc tgtgttcagg gccaagaacg tgcggaatga 660
ctggctggac ttgcgggttc ccatctggga ccaggacata cagtttctcc caggatcaca 720
gaagettgte acctgcacag ggtaccacca ggtccgtgtt tatgatccag catcccccca 780
gegeeggeea gteetagaga eeacetatgg agagtaceea etaacageea tgaceetcae 840
teegggagge aacteagtga ttgtgggaaa caeteatggg cagetggeag aaattgaeet 900
toggcaaggg cgtctactgg gctgtctgaa ggggctggca ggcagtgtgc gtgggttgca 960
gtgccaccct tcaaagcctc tactagcctc ctgtggcttg gacagagtct tgaggataca1020
caggatccag aatccacggg gtctggagca taaggtttat ctcaagtctc aattgaactg1080
ceteetettg teaggeaggg acaactggga ggatgageee caagageete aagaacceaal140
caaggtgccc ctagaagaca cagagacaga tgaactttgg gcatccttgg aggcagctgc1200
caagcggaag ctctcgggtt tggagcagcc ccaaggagct ctccaaacga gacggagaaa1260
gaagaagegg cetgggteea ceageceetg aegeceetgt geceaetttg taaataaact1320.
gctgaacacc caaaaaaaa gaaaaaaaa agggg
```

- (2) INFORMATION ON SEQ ID NO. 120:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1816 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```
ggtcagagag attctgaaaa gtaatccaaa gtgttccgta gctaaacatg gtgcaggctc 60
gttgtaccac tgcaaccgac tgacgttact gtagttccta gaatgctgtg agggcggggg 120
gttcagatca acataaagcc taacttgctg gagttgtagt ctcaaggctt tctctcttgc 180
ttaactaaaa cctaaggacc actgtttttg gtagcaatta tatggttact atccactgca 240
gtcctcagtt gttggggtaa atcccacatg gcagagtaag gcaccccaca gaaattaact 300
tggagageet gagaaattee cagtggeett ggeatagetg tetagaacae catetetagg 360
aaaatttaat totgtooctg gooagotatt gttottooac ttogttttot gotgtoocaa 420
ggccagatga gtggaatcac catctgactg ttgtcaataa aatgtatctg gcgtgaacag 480
caggataacc catgttetee acataaggat aaccttacgt gaaaccttee tgetgacaac 540
catgcagagg aatttttcca cttaagtcag agccttcctc cccatctgga attcacagct 600
gttecetgge ageacacagg agggtattaa ggacetttgt gaggetaggt acactgteca 660
cacctetttg gggaagttae gattttttt ttecateata atteagtete ttettattet 720
acagtgtgca ctttatgcct ctcgcctttt gataatagtt gttcagtgaa ggaagtcagc 780
tgccagaata ttaagaaggg tctcccttta tgtcagtaca actgttaggg cggccttccc 840
atttacttta ggtttcaaga ggattcaccg gaagcacatg ccccggtcta gtcccatttg 900
aaacagttct gctttactga gaccctaggc cggtctcctt gctgacccta gcgctgctgc 960
ctaggtgcca tttcctttcc tcctcagtca aatacaggct gcacattttg tcacttaatg1020
ccagtacaat ctgtgttact cctaaggact tttgggattt tgatgagacc tgcgagggag1080
aagacactga gaagccagtg atctgcaagc atttgctctt gtttccacat cacctctggg1140
atatttcage tgttgtttcc aaatggcaaa tcatcaacta aaagcacttg tttcaagttt1200
tgttctgcac tcccacgact gaagttgtag attgagctga ataaccatgg gaagtgaccal260
agcaaagaca ctcgattgga gtcagttgaa tatttgtacc ctcagtggag cccttctggt1320
cttttcttcc acttctgcag aatttcctct agcaaatact tctttctcct tgcttgcctc1380
caccatgata tttgaataag agatggccag aggataacac ttgtctctta aaaactaagc1440
taaaaaagaac ctagaacctt caattgagca gttgtgaaaa ttgctaatgg tgccaaggcc1500
aagcaaagag tttcagaaaa tgactgagaa ggagcgataa cccccagaat gcaaaatcag1560
gggcatcatt atccggtgct tgaacaagga gctccgctct acaactggtt tttttaggac1620
ttgtgaggaa cacagcaacg gaaatccatc cacaaaggat gcagtgcccc aacttgtact1680
gcgcctgaat agtcatgtga taatttactg aagaaatcta gtgtacttta aattttttc1740
ataaaagttt acattgtatt gtaggttaac attaaatgtt ttatagcaaa aacttcaaaa1800
aaaaaaaaa aaaaaa
                                                                 1816
```

- (2) INFORMATION ON SEQ ID NO. 123:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 740 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

tttagaattc agcataggtt gaggtcagaa agcaattcag gcatgagcca ccgtgcccgg 60 ctccacaccc atttcttaa aaaggatccc gtagcaggca gaaaagcccc ttccatcctg120 ctcctctgat actgtgcccc ctttggagata tttccgtcct ccacccacgt gtctgtggct180 ggaactgccc agcctgccc tggcccctg gaagcctccc cacagctggt aatctggact240 taaggattgc tgggccaccg cctctctgcc taccaccatt ccatatttaa gtggagcccc300 tacgtagaaa ggccccgggg ctttatttta gtctcctttt cagggatgtc gtggggggg360 gagggggttc ttggtgctac agccctctcc ccacccctaa agggacgccg acgctgtttg420 ctgccttcac cacatattag tgcttgaccc tggcagggga ccccatggaa aagatgggga480 agagcaaaat acatggagac gacgcacct ccaggatgct cgctgggatt cccacagag600 cgaataaagc caaggcttct tcccaaaaaa aaaaaaaaa aaaaaaaaa aagataggtt660 agttaaggcg gccgaaagtt tttttccctt tagtaagggt tagttttag tttggggttg720 gccttcgttt ttaagaacgt

- (2) INFORMATION ON SEQ ID NO. 124:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1493 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```
aacacctgcc ctcgttcagc gctttaggga gggcggctca ggcgccccgg agcaggcaga
gtgcgtggag ctgctgctgg ccctgggcga gcctgcggag gagctgtgcg aggagttcct 120
ggcgcacgcc cgcggccggc tggagaagga gctgagaaac ctggaggccg agctggggcc 180
ctcacctccg gctcccgacg tgttagagtt caccgaccat ggaggcagtg gcttcgtggg 240
eggeetetge eaggtggegg eggeetacea ggagetgttt geggeecagg geecageagg 300
tgccgagaag ctggcggcct tcgcccggca gctgggcagc cgctattttg cgctggtgga 360
geggeggetg gegeaggage agggtggtgg tgacaactea etgetggtge gggegetgga 420
cogettecae eggegettge gggetecegg ggeeetgetg geogetgeeg ggetegeaga 480
cgctgccacg gagatcgtgg aacgagtggc ccgcgagcgc ctgggccacc acctgcaggg 540
teteegggeg geetteetgg getgeetgae agaegteege eaggegetgg eageaecteg 600
cgtggctggg aaggaggcc ctggcctggc cgagttgctg gccaatgtgg ccagctccat 660
cctgagccac attaaggcct ctctggcagc agtgcacctt ttcaccgcca aagaggtgtc 720
ettetecaae aageestaet teeggggtga gttetgeagt cagggtgtee gtgagggest 780
catcgtgggc ttcgtccact ctatgtgcca gacggctcag agcttctgcg acagccctgg 840
ggagaagggg ggtgccacac cacctgccct gctcctgctg ctctcccgcc tctgcctgga 900
ctacgagacg gccaccatct cctacatcct cactctcact gatgaacagt ttctggtgca 960
ggatcagttc ccagtgacgc ccgtgagcac gctgtgtgca gaggccaggg aaacggcgcg1020
geggetgetg acceactacg tgaaggtgea gggeetggte atateaeaga tgetgegeaa1080
gagegtggag actegegaet ggeteageae tetggageee eggaatgtge gggeegteat1140
gaagegggtg gtggaggata ceaeegeeat egaegtgeag gtggggetee tgtacgaaga1200
gggtgttcgc aaggcccaga gcagcgactc cagcaagagg actttctccg tgtacagcag1260
ctctcggcag cagggccgct acgcccccag ctataccccc agtgccccga tggacaccaa1320
cctcttgagc aatatccaga agctattctc tgaacgtatt gatgtgttca gccctgtgga1380
gttcaacaag gtgtcggtgc tgaccggcat catcaagatc agcctgaaga cgcttgctgg1440
gagtgtgtgc gggctgcgaa ccittttggc cctttgcggg cttcaacaag ggg
```

- (2) INFORMATION ON SEQ ID NO. 125:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ccagactgaa ttgtcagtga gcggatctga gggcggtgtg gagtggccag tggggcttgg 60 ccgagatgga caaccggatt ccttatgatg actagccggt ggtttcttgc ctgcctatga120 ttgacccagt tttggcccga accatcacac tgaagaagcc tcctggagtc attgggatta240 agatcgaggg

(2) INFORMATION ON SEQ ID NO. 126:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1202 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```
tcggggggag cggcgggcg gcgcgggagt tggttctaaa gagtggtgag tcagaagaga
cgtcaggcag caagcgactt gggccatggc ctctgaccta gacttctcac ctccggaggt 120
geoegageee actitectgg agaacetget aeggtaegga etetteetgg gageeatett 180
ccageteate tgtgtgetgg ccateategt acceattece aagteecaeg aggeggagge 240
tgaaccgtct gagcccagaa gtgctgaggt gacgaggaag cccaaggctg ctgttccttc 300
tgtgaacaag aggcccaaga aagagactaa gaagaagcgg tagaagagga ggcctgagga 360
getgggeggg cagggagagg gtettgggga cageceteet gggaatetae attgtgttee 420
ecegeattee aggeteaggg tetgaggagg etgtgaegee etatgaeege agagatetag 480
acagtogtaa cagtococag getocagetg ggcaatocac caettoctet teettetget 540
tctgtgacgg tttagagtca agggggctga aacacactgt gagcatagac tgtattaggt 600
ttgttcagaa gccgggtcag ctcacagagt cacattttct tgcttagtca tgtgtccctc 660
cttgagttgc cccctccttg tgggtttaca ctacattttg gagtcattgt ctaatgctga 720
caagcacacc ctctcccatt atttgtgcac tacagatctc ctgctgatca gtcacctttg 780
ttgctgctgt gtagacagag ccaggcctca cctgtttgtt taggccaaga tgccatggac 840
atgcagcgtt agtgatccca ctagctgtga cagccaggcc cagaaaatgc ctggcgtgag 900
agccagcaga cagccaggcc aggggtaggc agtgcctgct tctgctccat caggtgcagg 960
ggatttggct gaaggcgtgc atatttcctg ggcacaaact tcctgagcct ctgaaatggg1020
aggetegtea attteagace aacetetttt caacecatea tageaegtte aaggtgtgcc1080
tittactict acctgtacat cocccatece ticaattett teattecetg accagtgagal140
```

- (2) INFORMATION ON SEQ ID NO. 127:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1014 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

cccttttttt ttcttttga gatggggga aagtcctagc aaaaggcagg agttagcatt ttcctttaac aagactttct aatgctaaac aaagaccaac ttcttttaaa aggggttgtt 120 ttggttgtgg gtgaaaaata ctgtactgta atgatctgct tggttttaaa gcaaaagaga 180 tectgacatg tgaaaccaat acaccaaaat gecaagteea caaatgaaca aaacaagtge 240 ttaaaaaaaa aattottotg otottatatt tttggaggaa gotgotgatt ttggotgtoa 300 gatttcactt agaaatggtc actttctgag atgctttttc ctcacagaat ctgtagataa 360 acticattaaa agattgtccc atttcaaaat cacccccaag tctagcagca ctgtttttt 420 tttttttagt ttttgtttta aaattacaaa ccaagtaaga agtccaacat cctcttccat 480 gaacagettt gtgacagage teetgagtgt gtgeageece caetgtgete tqaatacagt 540 ctctgcagct ccagtgtgtc ctcttttcag gaaggaaagc atattcaata cattcactat 600 ctgtaccccc tggaacttgc acatgctgac gagctattat aagccaactc atccccagct 660 ctcttccggg actggtcacc ccttgtaaaa ccattctgta taagttctct ttgaaatttc 720 tgatcttgag cagcatattc agaaagttca gattccaccg ccggagggag aatgtttgga 780 ataaatttag aaaatagagt tggagccatc tgaacccact ctggtctgag ggtatacagg 840 cctttcacaa tatttgccat agttgaaggt gtgacctgaa atggtgttga ctgggcttct 900 aaaagtaaag gcattaggcc gtaaatgtgc ttttctgcaa catgttccgt aaacagcttt 960 ataagggcac ctttaagccc gggtaagctg gtccatggga acctatcgtt tttq

- (2) INFORMATION ON SEQ ID NO. 128:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1171 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```
caccaaatta atcaggttta cagacagggt cccaccggta ttcacattct tgttagtgat
cagatggttc agaattttca agatgagagt tgttttttat tctccacagt aaaagctgaa 120
agtagtgatg gcatccacat aattttgaaa tgatgtctta tatagactga actgtattca 180
gtaccaaata gtcacgctta aaagtgtgtg aagactgaat ccaagaagtc ttgggattgg 240
attttaccat atgaaatgtt tcatattgaa aacacaagat gacctttcta atgagctgta 300
tgaqaggtga atctcctcac tgtcactgcc atagccaagc atcctcatga gagtgagcac 360
atcggcacag catgcatcca gctctggagg ccacggtgca ggcatagctg cctgctgctc 420
tggcagaggc cagtaaatac agttcctaga agcagccttt gctgtctttt tacactgtat 480
gcggtttgga aatgaatgta gaaacttact gtgggcattt acctttctgt gccagtttgg 540
cttttattgc ctgaacctta tgctgacctg gagaggagat gggggacagt gctgttgtgg 600
ggccagcagt gaatctgtat gcggagagtt gtgttgtgct gatgtggccg ttggtggtca 660
ggtaagagge teggeacett ettggaagaa atcatgtetg agggtgtaeg tttgatatga 720
tcatgccaga ttggagaaga tccaagccag gaagatgggc ttgaagcaaa ctgcattatc 780
aggagtacct tggtgagagg atcagtgtaa atcctaatag gtacaaagac ttttgtgttt 840
tggctttgtc acagatttat tgaaaaactt ttttgcttct gcttccattt ttagcatttt 900
agtttctggt tttcattttt ggagattcct tgccttttaa actcgtggtt tttctctcat 960
tttcttccct ctctccctcc atctctgacc acccccaccc taacccccca cccccaccat1020
cctattaaac atttttaaag ccctacccca gacattggga aataggtgga cccaagtagg1080
gggggaggaa agtattgatt tgtttggata ggcttgtgga ttagggtgtt aaggggttct1140
tggattatgg aacaaggtgg aattttttt g
```

- (2) INFORMATION ON SEQ ID NO. 129:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```
ggccgggacg cagggcaaag cgagccatgg ctgtctacgt cgggatgctg cgcctgggga 60 ggctgtgcg cgggagctcg ggggtgctgg gggcccgggc cgccctctct cggagttggc120 aggaagccag gttgcagggt gtccgcttcc tcagttccag agaggtggat cgcatggtct180 ccacgccat cggaggcctc agctacgttc aggggtgcac caaaaagcat cttaacagca240 agactgtggg ccagtgcct aggttgacct ttgcccaact caaggaggg tcg 353
```

- (2) INFORMATION ON SEQ ID NO. 130:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 205 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

cggctgagcg gccccgcagc caacccccga ggagcggccg gctggcgtgc cgctggcgcc 60 caggagttgg ggatgtccta caaacccatg cgccctggc tgcccagcag caccccctgg120 tctgccaggc accccctggg gcccggggca ccccggttcc ctgacaggga ggcgtgcgcg180 tgcgccgtgc ggggctgcag tgtcc

- (2) INFORMATION ON SEQ ID NO. 131:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 211 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

aaatcacctt acaacccatt tctcagaaca tgtttctatt gttaaacaac acacaactat 60 tttatttatg tgttttattt atgcctgatc accaatatca ataactgaaa cacagcagtt120 tagtaataat ttaatacaca ccataacctg cctattgaga atggcattat atttgttttc180 attgtagtgg ctccatccaa aataaaatga t

- (2) INFORMATION ON SEQ ID NO. 132:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 867 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

gtcttcccaa gatggagatg ctaacgaaac tgagaagggg gcgtatgttt gacgaaggtt 60 tgtgcaagtc aggcccttct ggaacacagc agggcctaca acgaggggcc tttgcgatgg120 gctgtgagga tgggggggt gggaagaatt ggccacgtta gagaccccat gccaccccac180 catggtgagt gctctgtgcc tcctgctcac ctgtggtgag tgggcgagct gggcgagctg240 ggcgagctgg gctggggaga gcctgtgagg accgagagag gaaatgagaa gaaggaacaa300 aaatatatt tctatgtaat ttatattta cttatgccaa attattatg ataatttgcc360 attgccatag taggatgcac cgcaggccc tggccactga aagatgtgat ttgtgaggct420 tgtccctatg taggatgcac cgccaaaagg tggctttgcc ataggaggaa tggaatgtt ttccccaatg tggctttgcc tcaagcaacc taccctgatg540 ttttactcat tggaatgtt ttccccgatt gtggatgact tctttctga tggagaggt600 catcttcagg cctgaagctg cacgacctga agttcgcctg catttatcag cctgaagctg cacgacctga ggttcctgc tggcacatg tgtggttgt gcatgttga780 gcagaaggga ggatgagaa aaaagagaag gaaaccccg ttagtgacaa gtgtttttt840 gagttgccag gttttgccat cattaaa

- (2) INFORMATION ON SEQ ID NO. 133:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

aattcagact cccattctta acttggcatt tttgtagctt acaggaacca gcttggtgta 60 ccttctctta tgagatgcag ctggaaagcc atttatgcaa gaggtggttt cacttttgtc120 gctcctccat tcattgaccc ttcagccttt aaaaaaattag aatgtgaaaa ttagtagcaa180 agagtgcaga gatattagct taagggataa ataaatgaaa gtagcaagta gctcattatt240 tatgaagagt aataatt

- (2) INFORMATION ON SEQ ID NO. 134:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

gactggctca tggcctctgt aaatggctgc tggcgggact gtctgcctag cgggtgccct 60 tggaacctag cccttggtgg gttttgagga aatgattcct gaatgaggag tcgattgccg120 tgtgaagggc tggtggcacg gcacccgcgt gagctacgcg tgccctcagt gcgcttctgg180 attgactggc catgggtgct caca

- (2) INFORMATION ON SEQ ID NO. 135:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 245 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ttgcaccatg gtaaacgtgg ataatacagt atcatttttg agcagttttt taaatgtaaa 60 tctgtatctt actcagagtg tgtgtctgaa gttattaagg acatttccca acgttactgg120 cccatttccc tttgtaatca gaggaattct gtttcaagat tattgttgtg tgtgatctgt180 ggctcttgat cagaatgaag ttaaatggcc acaggaggat taagctatga ggttggcatt240 tttca

- (2) INFORMATION ON SEQ ID NO. 136:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1637 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```
ggggagggac gagtatggaa ccctgaaggt agcaagtcca ggcactggcc tgaccatccg 60
getecetggg caccaagtee caggeaggag cagetgtttt ceatecette ceagacaage 120
tctattttta tcacaatgac ctttagagag gtctcccagg ccagctcaag gtgtcccact 180
atcccctctg gagggaagag gcaggaaaat tctccccggg tccctgtcat gctactttct 240
ccatcccagt tcagactgtc caggacatct tatctgcagc cataagagaa ttataaggca 300
gtgatttccc ttaggcccag gacttgggcc tccagctcat ctgttccttc tgggcccatt 360
catggcaggt totgggctca aagctgaact ggggagagaa gagatacaga gctaccatgt 420
gactttacct gattgccctc agtttggggt tgcttattgg gaaagagaga gacaaagagt 480
tacttgttac gggaaatatg aaaagcatgg ccaggatgca tagaggagat tctagcaggg 540
gacaggattg gctcagatga cccctgaggg ctcttccagt cttgaaatgc attccatgat 600
attaggaagt cgggggtggg tggtggtggt gggctagttg ggtttgaatt taggggccga 660
tgagcttggg tacgtgagca gggtgttaag ttagggtctg cctgtatttc tggtcccctt 720
ggaaatgtcc ccttcttcag tgtcagacct cagtcccagt gtccatatcg tgcccagaaa 780
agtagacatt atcetgeece atecetteec cagtgeacte tgacetaget agtgeetggt 840
gcccagtgac ctgggggagc ctggctgcag gccctcactg gttccctaaa ccttggtggc 900
tgtgattcag gtccccaggg gggactcagg gaggaatatg gctgagttct gtagtttcca 960
gagttggctg gtagagcctt ctagaggttc agaatattag cttcaggatc agctgggggt1020
atggaattgg ctgaggatca aacgtatgta ggtgaaagga taccaggatg ttgctaaagg1080
tgagggacag tttgggtttg ggacttacca gggtgatgtt agatctggaa cccccaagtg1140
aggetggagg gagttaaggt cagtatggaa gatagggttg ggacagggtg etttggaatg1200
aaagagtgac cttagagggc tccttgggcc tcaggaatgc tcctgctgct gtgaagatgal260
gaaggtgctc ttactcagtt aatgatgagt gactatattt accaaagccc ctacctgctg1320
ctgggtccct tgtagcacag gagactgggg ctaagggccc ctcccaggga agggacaccal380
teaggeetet ggetgaggea gtageataga ggatecattt etacetgeat tteecagagg1440
actagoagga ggcagoottg agaaacoggo agttoccaag coagogootg gotgttotot1500
cattgtcact gccctctccc caacctctcc tctaacccac tagagattgc ctgtgtcctg1560
ectettgeet ettgtagaat geagetetgg eceteaataa atgetteetg eatteatetg1620
caaaaaaaa aattttc
```

- (2) INFORMATION ON SEQ ID NO. 137:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

aaaagcatag ctcactctgt aataggctat tttcatgatt tcaagtggtt ttatgaagaa 60 acagaaagca gtgatgatgt tgaagtgctg actctcaaga aattcaaagg agacctggccl20 tacagacgac aagagtatca ggtagaattc aacatatggt gcttgaagtg ggctcttgtt180 ttatcagtta tggcatatgt aaataacagt gtaccaagtt agtgtggtgt ttatgaagat240 gagtttaatc ttttgtgatg

- (2) INFORMATION ON SEQ ID NO. 138:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 957 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

ggggaatttg tetttggaaa gettgtgeaa eetetacaae tggegataca agaatetagg 60 aaacttaccc catgtgcagc tcttgccaga gtttagtaca gcaaatgctg gcttactgta120 tgacttccag ctcattaatg ttgaagattt tcaaggagtg ggagaatctg aacctaatcc180 ttacttctat cagaatcttg gagaggcaga atatgtagta gcacttttta tgtacatgtg240 tttacttggt taccctgctg acaaaatcag tattctaaca acatataatg gccaaaagca300 tcttattcgc gacatcatca atagacgatg tggaaacaat ccattgattg gaagaccaaa360 caaggtgaca actgttgata gatttcaagg tcaacagaat gactatattc ttctttctct420 ggtacgaacc agggcagtgg gccatctgag ggatgtccgt cgcttggtag tggccatgtc480 tagagccaga cttggacttt atatcttcgc cagagtatcc ctcttccaaa actgttttga540 actgactcca gctttcagtc agctcacagc tcgcccctt catttgcata taattccaac600 agaacctttc ccaactacta gaaagaatgg agagagacca tctcatgaag tacaaataat660 aaaaaatatg ccccagatgg caaactttgt atacaacatg tacatgcatt tgatacagac720 tacacatcat tatcatcaga ctttattaca actaccacct gctatggtag aagagggtga780 ggaagttcaa aatcaagaaa cagagttgga aacagaagaa gaggccatga ctgttcaagc840 tgacatcata cccagtccaa cagacaccag ctgccgtcaa gaaactccag cctttgagcg900 tgagagccgc cccggtgggg aaggggcaat tgcgttgggg gggcttgggt gtttttt

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 760 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

- (2) INFORMATION ON SEQ ID NO. 140:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

aggaaccctc cggcctagaa gttcagatgt cttgccaata tatctgtgct tcacaacttg 60 cctactctct ctgaccccta acattttcac atacttttcc aattctgcct gtcataaatt120 tgctgcttcc ccctaagtag aatgttgatt cctgtcaaac acacagccta gccctgattc180 ctcctcttct ctcaagcagt gatattgtca acaatgataa acaactacta tgtactgagt240 gtttttttat gtgctgctca cactttatac acatgtatag

- (2) INFORMATION ON SEQ ID NO. 142:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: Nucleic acid

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

gcggccgctc gagggaagca cccgccggtt ggccgaagtc cacgaagccg ccctctgcta 60 gggaaaaccc ctggttctcc atgccacacc tctctccagg tgccctctgc ctcttcaccc120 cacaagaagc cttatcctac gtccttctct ccatctatcg gaccccagtt tccatcacta180 tctccagaga tgtagctatt atgcgcccgt ctacaggggg tgcccgacga tgacggtgcc240 tcgcagtca aattactctt cgggtcccaa ggtttggctt tcacgcgctc cattgccccg300 gcgtggcagg ccattccaag cccttccggg ctggaactgg tgtcggagga gcctcgggtg360 tatcgtacgc cctggtttg gtgttgcctc actcctctga gctcttcttt ctgatcaagc420 cctgcttaaa gttaaataaa atagaatgaa tgatacccg g

- (2) INFORMATION ON SEQ ID NO. 143:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 436 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

caaagatgte atgtggcag aatcatett tagteteace actecacat gatggtcaca 60 tagaggtgtg agttgggaag ttgttaaata caagagggtt tgagettetg gagaagaggg120 aaatgtaaaa gtattttte etttaagaaa gataaaaagg taageetaaa eetttggegge180 cacegaagte agetgttaeg eatgtgtagt taaattteae tgtaaatatt teataagggt240 tettagaatg gagecaggtt gacateacag eeceaactgt aceaaaggaa eeattteea aagaaacaeg aatgtetatg geagagttaa eataaggtea360 gaaaateete tggaagaaat tteggtatea atgtttataa teetetgeatt taggggtttg420 eeagtttggg eaaaaa

- (2) INFORMATION ON SEQ ID NO. 144:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 287 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

ctttaaagta gggctgtgga agggggatat agtagaggg gagagggctg ttttatacac 60 gtataaatgg tatacaccat ttatacacgg tggtcagaga agctctgatc aggtgacgta120 tgtacagaaa gtcactgtgg cctgagtaga gtcaaggaga aggagcagca agagttgagc180 ttagggaggt ggagaaggg tggaatagat caagcaagac cttggccctg gtagggatct240 gggatttaaa gtgagaggac aaccgttggg atgttgtgag cacagaa 287

- (2) INFORMATION ON SEQ ID NO. 145:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

ggcgacgcct cggtactgac ctctgcagag ccgggtggag cccattgacg tccagcgaac 60 gaggagcagc gatgacggt cgggtgcagc tgataaaggc cctctggcc ttgccgatcc120 ggcctgcgac gcgtcgctg aggaacccga ttccctttcc cgagacgtt gacggcgata180 ccgaccgact cccggagttc atcgtgcaga cgggctccta catgttcgtg gacgagaaca240 cgttctccag cgacgcctg aaggtgacgt tcctcatcac ccgcctcaca gggcccgcc300 tgcagtggt gatccctac atcaagaagg agagcccct cctcaatgat taccggggct360 ttctggccga gatgaagca gtctttggat gggaggagga cgaggacttc taggccggga420 gaccctcggg cctggggcg ggtgctctg ggagggtccg ctgtgttact ggccgccgcc480 agggtcgca ccggcgcc ccctccgcg gtcctcccc cctcaaaccg ccgcgaagtc540 ccctgcggtg

- (2) INFORMATION ON SEQ ID NO. 146:
 - (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1790 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
 - (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

anthanaaa	, cagggagtet					
caccataca	g cagggacce	- ccggcccagg	j cagccgggac	ccagccagco	ctgcgcctcg	60
cycegrege	g catgegreet	ggtctttctc	: tagagttgta	i tatatagaad	atcctggagt	120
ccaccatgaa	cggacagttg	gatctaagto	ggaagctaat	Catcasaget	caacttgggg	100
	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	· ~ · · · · · · · · · · · · · · · · · ·	l aagararrac	·		
J J	,	- 444666CLL	: coaoraarda	F/3334+334-		
J - J J -			LIGATAGETC			
agtgcagtag	gatactgaaa	ctgacattat	ttattaataa	. cgaccittcc	cccttgaat	360
caagtcaggt	gaaatatoto	Catcaagaac	toatacaacy	taanaan	gtgaatcgtt	420
tattggatag	cttqqaacca	Cotogagaac	Cacagaact	ccgaaataaa	gtgaatcgtt cctgaaaatg	480
atactgtgga	tootagggaa	gaaaagtetg	caggaccttc	caccaatatt	cctgaaaatg	540
aggttatggc	agcaagtato	tetactttta	atcottant	ccctggaaaa	cagtctactc	600
aaaatottat	gtcagcgttt	gacttaacag	attettada	aaaccaagat	gaaatcaata	660
ctgcagaaga	togttcagga	acaccccacag	acgatcaggt	ttcagggcca	gaaatcaata cccagtgctc	720
caccaggggt	tcaccacac	Caccogaca	geattgette	ctcctcctca	gcagctcacc	780
ttgaaggtca	gatgtaccaa	Cagtaccat	acacaggage	tcagactcaa	gcagctcacc	840
3 3 3	33	- Curicaccauc	aacaddccaa	CESEGGEGGG		
			- ULAL FCACTA	TTC3~~~~	_	
		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	accoratates	~~~~~~~		
		446646666	aacaacrocc	TOCTORGO -		
		9000000	acactocca			
		Caaccccaa	ECCCCCAAC	CC3300ta		
		uuaa	uraccardac	CCCTTCCTCCC		
	3-3		OF CAMMORES	Taggggggg		
		ucuccaatta	alucadetde	T = 000 t = t = 0		
,			JAAGEECAGA			–
,		9	adiaratre	7CT777777		
J		you caaaa.	uladcadetr	<b>でたたっぺたたっぺた</b>		
		4 C C G G C C C G G	CLEECTACCE	TCCC++~+~-		
		auccatch La	CECOOCTEE	<b>アコクセッセヒッッ・</b>		
J J J		aayatat	Latutataaa	ALGEARCACE	~~+~~+~~+3:	740
taataaagat	gattgaatcc	aaaaaaaa	aaaaaaaaa	aaaaaaaaa	1'	7 <b>9</b> 0
•						, 30

- (2) INFORMATION ON SEQ ID NO. 147:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 2357 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

			and the second s			
ctcgagccga	atcggctcga	gcgcagacct	gcagcgggca	aagagctccc	gaggaagcac	60
agcttgggt	: aggttcttgc	: ctttcttaat	: gttagagaca	gctaccogaa	ggaggggaac	120
aaggagttc	. Cttccgcago	ccctttccc	: acgcccaccc	ccagtctcca	gggaccettg	180
derdeereer	. aggctggaag	ccatggtccc	: gaagtgtagg	gcaagggtgc	ctcaggacct	240
tttggtcttd	agcctccctc	agcccccago	atctgggtta	gatagegact	cctocctact	300
	agacyccca	gageetteea	Loacetecce	: tccccaaccc	33+GGGGGGG	360
3346663346	, ctycacaaay	Leageaddda	ccactaaatc	tccaadacct	artatacas.	420
33003300	. egualgeelg	Laggigication	i acacocaaot	atatasatat	asatatasas	400
33333-33	, 9990909000	graggratet	ctaaacctat	- atataaataa	aattatataa	540
33333	agecycece	Courgagage	ttcctcagaa	CCCacactca	G3GGGGGGGG	600
	. ayayaayıtt	CLLAGGLEET	ctttagaata	' aaattcctcc	ttcccccc	660
	ayyaayccca	Claatiligee	ctttacaata	tacadaataa	3300t 3300	720
999-9-99	agilygggcl	gucalagggt	ctacaaccta	ctadaactaa	acaataasaa	780
aaggeeeege	cactctagge	atatytttcc	ccatctctgt	ctagaactac	agaatagggt	910
ggcagaagcg	ccaccccgcg	ggigiciccc	tcaaaaactc	- Etecectada	cctcccctc	200
actiacataa	ageteetteg	aagcaagaaa	gagggtccca	gggctgcaaa	actoraacoa	960
cageceeggg	garggggagg	yaaayacggt	gctatatcca	gtteetacte	tctactcata1	020
99-999-9	acaacccccgg	cultactiga	ttcatctctc	- atttttcttac	caccetetee1	000
gagececae	cccattttta	Lucique	aaccaggeee	taccattacc	ctcttataaa1	1 40
ceggeacacc	rgcacccaca	ggrgagggc	aggacctgaa	ggtattggcc	tottcaacaa1	200
ccagccacca	raggigitit	tyttaactgc	ttgttaattg	atttggggat	gtttgccccq1	260
aacgagaggc	cyayyaaaay	actytyggtg	gggaggcct	gcctgaccca	tcccttttcc1	320
ccccggccc	cagcccaggc	ggaggcaagt	ggaatatett	atattqqqqq	atttgggggg1	300
	agagaattt	Ligggagtet	tadataacac	tagtacatta	toffttcctc+1	440
-gacccaaa	gcacaacgcg	gatttgggga	ccaaaggtca	gggacacatc	cccttagagg1	500
accegageee	gggagagcgg	Lyaylygaag	ggaggagcag	Caadaadcad	CCtCttttc1	560
cccagcccaa		LagalaaggC	aadccadtca	tagaatetta	ctgcaggggal	620
coccccacc	ceeeegeee	raaaaalagg	ggccgttttc	ttacacaccc	CCadadadad1	600
gagggaccgc	cacactygig	cigagigacc	gggggctact	aaacatctat	totttaccas1	7.40
aaccaccac	ccctagaaga	yearagagee	ctgaggggct	agactagact	gggctgaggg1	900
corggeoree	cccacagecc	acagaggece	ttcagctcat	ttaatcccad	Gaaagagggal!	860
coaaagccag	aacgcgaaca	Laactitigt	ggaccaatac	taagaataac	aagaagecea1	920
9-99-94994	aagigigiii	Luccaguage	gcctcctatt	tteteestet	catotecete19	200
cayyyaaaat	gactitating	Citaattict	geettteece	cotcacacat	acacttttac2	340
9000000000	acayciyyaa	aaaacaaat	accaccetae	aaacctgtat	######################################	100
acagaaacga	ccacytyaaa	rrigiditata	tccaaacatt	tcatccatat	$\alpha$ t at $\alpha$ t $\alpha$ t at $1$	160
3-3-3-3-3-6	gegegaagee	yccagiccat	ctttttatat	aaaattatta	totoatttta21	220
geeegeeeg	geceeeeee	ccycyggctt	gtgctcggca	CCaaagagaa	aaacotttta21	200
9999000904	acceaeceeg	aaaaatttaa	ctttgagcga	aaaggggag	tgttttaccg23	340
tąggggggta	aaataaa				23	357

- (2) INFORMATION ON SEQ ID NO. 148:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 907 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

gttcattgtc tggcaccaag ctccttgggg tgaattttct tccaaaagag tccggggagt 60 ccaggteett etteetggtt acteataacg eggeeceatt teteacteec attgggegte120 gggtttctag agaagccaat cagtgtcgcc gcagttccca ggttctaaag tcccacgcac180 eccgegggae teatattttt eccagaegeg gaggttgggg teatggegee eegaageete240 ctcctgctgc tctcaggggc cctggccctg accgatactt gggcgggtga gtgcggggtc300 cagagagaaa cggcctctgt ggggaggagt gaggggcccg cccggtgggg gcgcaggact360 cagggageeg egeceggagg agggtetgge gggteteage eceteetege ececaggete420 ccacteettg aggtatttca geacegetgt gtegeggece ggeeggggg ageceegeta480 categoogtg gagtacgtag acgacacgca attectgegg ttegacageg acgeegegat540 tecgaggatg gageegeggg ageegtgggt ggageaagag gggeegeagt attgggagtg600 gaccacaggg tacgccaagg ccaacgcaca gactgaccga gtggccctga ggaacctgct660 ccgccgctac aaccagagcg aggctggtga gtgaacccgg ccgggggcgc aggtcacgag720 cacccccat ccggcacggg accgcccggg tccttcagag ttccgggtgc gaaatgtacc780 ccgagggagg ggaggcgttg gattgctgga gtggatactg ggggggtttt acgcaggttc840 attttcagtt taggccaaaa tccccgcggg ttgggcgggg atgggggggg gttaggtggg900 cggggtt 907

- (2) INFORMATION ON SEQ ID NO. 149:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1987 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```
aggaggcgtg ggggggggg cgggggagtc agggaagagc accatcgtca agcagatgaa
gatcatccac gaggatggct actccgagga ggaatgccgg cagtaccggg cggttgtcta 120
cagcaacacc atccagtcca tcatggccat tgtcaaagcc atgggcaacc tgcagatcga 180
ctttgccgac ccctccagag cggacgacgc caggcagcta tttgcactgt cctgcaccgc 240
cqaggagcaa ggcgtgctcc ctgatgacct gtccggcgtc atccggaggc tctgggctga 300
ccatggtgtg caggcctgct ttggccgctc aagggaatac cagctcaacg actcagctgc 360
ctactacctg aacgacctgg agcgtattgc acagagtgac tacatcccca cacagcaaga 420
tgtgctacgg acccgcgtaa agaccacggg gatcgtggag acacacttca ccttcaagga 480
cctacacttc aagatgtttg atgtgggtgg tcagcggtct gagcggaaga agtggatcca 540
ctgctttgag ggcgtcacag ccatcatctt ctgcgtagct tgagcgccta tgacttggtg 600
ctagctgagg acgaggagat gaaccgcatg catgagagca tgaagctatt cgatagcatc 660
tgcaacaaca agtggttcac agacacgtcc atcatcctct tcctcaacaa gaaggacctg 720
tttgaggaga agatcacaca cagtcccctg accatctgct tccctgagta cacaggggcc 780
aacaaatatg atgaggcagc cagctacatc cagagtaagt ttgaggacct gaataagcgc 840
aaagacacca aggagateta cacgcactte acgtgcgcca ccgacaccaa gaacgtgcag 900
ttcgtgtttg acgccgtcac cgatgtcatc atcaagaaca acctgaagga ctgcggcctc 960
ttctgagggg cagcggggcc tggcgggatg ggccaccgcc gactttgtac cccccaaccc1020
ctgaggaaga tgggggcaag aagatcacgc tccccgcctg ttcccccgcc gcttttctcc1080
tettteetet etttgttete ageteeeet gteeeeteag etceagaegt aggggagggg1140
ttgccacagg cctccctgtt tgaagcctgc ccttgtctga gatgctggta atggccatgg1200
tacccccttc tgggcatctg ttctggtttt taaccattgt cttgttctgt gatgaggggal260
ggggggcaca tgctgagtct cccaaggctg cgtctggagg ggcccctgct tctccagcct1320
ggacccccag ctttgcccaa caccagcccc tgccccagcc caagtccaaa tgtttacagg1380
gagecteetg eccagteece caaceceage egeteggagg ecceaaagga aaaagcacaal440
gaagegtgag aegecaceat teetggaaae caeagteeae etgeteatte tegtagettt1500
ttaaaaaaat gaaagtaaag gaaaaaaaaa aaactgcaaa tctagaaaac tttttagaga1560
aaaactattt aaaactgtca gatcctgacc agcaagcgcc cccccagccc cccttccaag1620
tgactccgtg ccttgagtgt gtctgcgtgt ttacacccgt ccctctgctg gccgccccg1680
tgcgagcggc accectgece tgccctecae agaattgggt tecaaggget gttecagaca1740
actgecaacg teactgaggg ecetgeeeca geggeeetgg ececaggete tattaaceta1800
aaatgtaget eeetageget aacetaggaa eegeegetge etgetggggg geeaegeeee1860
tcatgccctt gtcccaggcc cggggccttc agcgttgaac acttccttgc ttttttcaca1920
```

## (2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2906 base pairs
  - (B) TYPE: Nucleic acid (C) STRAND: individual

    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

gtccagaagc aaaaattaag ttccccaagt tttccatgcc caagatcggc atcccaggtg tgaaaatggg gggtggggga gccgaggtcc atgcccagct accctctctt gaaggagact 120 tgagaggacc agatgttaag ctcgaagggc ccgatgtttc tctaaagggg ccaggagtag 180 acttgccttc agtgaacctc tctatgccaa aagtctctgg gcctgacctt gatctgaact 240 tgaaaggacc aagtttgaag ggagacctgg atgcatctgt teecagcatg aaggtgeatg 300 ctccagggct caacctcagt ggtgtcggtg gcaaaatgca ggtgggagga gacggtgtga 360 aagtgccagg gatcgatgcc acaacaaagc ttaacgttgg ggcaccagat gtgacactga 420 ggggaccaag cctgcaggga gatctggctg tctctggtga catcaaatgc cctaaagtat 480 ccgtaggagc tcctgatcta agcttggagg catccgaagg cagcattaaa cttcccaaaa 540 tgaagetgee ccaatttgge atetetaete eggggteega ettgeaegte aatgeeaagg 600 ggccacaggt ttctggcgaa ctgaaggggc caggtgtgga tgtgaacctg aaagggcctc 660 ggatttcagc accgaatgtg gactttaact tggaaggacc aaaagtgaaa gggagccttg 720 gggccactgg tgagatcaaa ggccccactg tcggaggagg tcttccaggc attggtgttc 780 aaggeetaga aggaaacete cagatgeetg gaattaagte etetggatgt gatgtgaace 840 tgccaggcgt gaatgtgaaa ctcccaactg ggcagatttc tgggcctgaa atcaaaggtg 900 gtotgaaagg ttoagaagta ggtttocatg gggotgotoc tgatatoagt gtgaaggggo 960 ctgcctttaa tatggcatct cctgagtcag attttggcat caacttgaag ggcccaaaaa1020 tcaaaggagg tgcggatgtt tcagggggtg tcagtgcccc agacatcagc cttggtgaag1080 ggcatttgag tgttaaaggt tccgggggtg agtggaaggg accccaagtc tcctctgctc1140 tcaacttgga cacatctaag tttgctgggg gccttcattt ctcaggacca aaggtggaag1200 gaggtgtgaa aggaggtcag attggactcc aggctcctgg gctgagtgtg tctgggcctc1260 aaggtcactt ggaaagtgga tctggaaaag taacattccc taaaatgaag atccccaaat1320 ttaccttctc tggccgtgag ctggttggca gagaaatggg ggtggatgtt cacttcccta1380 aagcagaggc cagcatccaa gctggtgctg gagacggcga gtgggaagag tctgaagtcal440 aactgaaaaa gtccaagatc aaaatgccca agtttaattt ttccaaacct aaagggaaag1500 gtggtgtcac tggctcacca gaagcatcaa tttctgggtc caaaggtgac ctgaaaagtt1560 caaaggccag cctgggctct ctggaaggag aggcagaggc cgaagcctct tcaccgaaag1620 gcaaattctc cttatttaaa agtaagaagc cacggcaccg ctcaaattca ttcagtgatg1680 aaagagagtt ctctggacct tccaccccga cggggacgct ggagtttgaa ggtggggaag1740 tgtctctgga aggtgggaaa gttaaaggga aacacgggaa gctgaaattc ggtacctttg1800 gtggattggg gtcaaagagc aaaggtcatt atgaggtgac tgggagcgat gatgagacag1860 gcaagttaca ggggagtggg gtgtccctgg cctctaagaa gtcccgactg tcctcctctt1920 ctagcaatga cagtgggaat aaggttggca tccagcttcc cgaggtggag ctgtcagttt1980 ccacaaagaa agagtagcag gcctttgtag aacaaaacat cagccttggg tggtgttc2040 ctatataaac tccaaaggga aacacccga ctgcctcagc aatcatgcaa agaccttgcc2100 tggcccggtg gcaagcgctg aaaaaccgac cgcctgtagg ctcctggaac tatacagata2160 ggtaaagagt tccaagttcg tccagcccat gtgcaaagtc aacagtattt gccttaagat2220 ttcatatata tatattttt tgcattgact gctgagagct cctgtttact aagcaagctt2280 ttgtgtttat tatcctcatt tttactgaac attgttagtt ttggggtaat ggaaacccac2340 tttttcattg taatgacttt gggggctttt gttagtaagg gtgggtgggg tgatgggttg2400 cagacggagg tcaggtcttc ctctttcctg agactggatc tgttcaaaca gcaaacgccc2460 acagatggcc cagaggtggt ggtagtcagg gtgtgtgggt gtttttaggg ttctttagtg2520 ttgtttcttt cacccagggg tggtggtccc agccagtttg gtgctgacgg tgagaggaaa2580 ttagaatctg tttgcaaatt gtccaaccca cccctcaac atgaggggct tccattttct2640 gtgttttgta agggaactgt ttccttcatg ccgccatgtt cctgatatta gttctgattt2700 ctttttaaca aatgttatca tgattaagaa aatttccagc actttaatgg ccaattaact2760 gagaatgtaa gaaaattgat gctgtacaag gcaaataaag ctgtttatta accttgaaaa2820 agggaggaa aggggggggg gggagg. 2906

### (2) INFORMATION ON SEQ ID NO. 153:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2367 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```
gesteeegee egeogestet gteteestet etecacaaac tgeeeaggag tgagtagetg 60
ctttcggtcc gccggacaca ccggacagat agacgtgcgg acggcccacc accccagccc 120
gecaactagt cageetgege etggegeete cectetecag gtecateege catgtggeee 180
ctqtqqcqcc tcqtqtctct qctqqccctq aqccaqqccc tqccctttqa qcaqaqaqqc 240
ttctqqqact tcaccctgga cgatgqqcca ttcatgatga acgatgagga aqcttcgggc 300
getgacacet egggegteet ggaceeggae tetgteaeae ecacetacag egecatgtgt 360
cetttegget gecaetgeca cetgegggtg gtteagtget eegaeetggg tetgaagtet 420
qtqcccaaaq agatctcccc tgacaccacg ctgctggacc tgcagaacaa cgacatctcc 480
gageteegea aggatgaett caagggtete cageacetet aegeeetegt cetggtgaac 540
aacaagatet ecaagateea tgagaaggee tteageeeae tgeggaaget geagaagete 600
tacateteca agaaccacet ggtggagate eegeecaace tacecagete eetggtggag 660
ctccgcatcc acgacaaccg catccgcaag gtgcccaagg gagtgttcag tgggctccgg 720
aacatgaact gcatcgagat gggcgggaac ccactggaga acagtggctt tgaacctgga 780
geettegatg geetgaaget caactacetg egeateteag aggeeaaget gaetggeate 840
cccaaagacc tccctgagac cctgaatgaa ctccacctag accacaacaa aatccaggcc 900
atcgaactgg aggacctgct tcgctactcc aagctgtaca ggctgggcct aggccacaac 960
cagatcagga tgatcgagaa cgggagcctg agcttcctgc ccaccctccg ggagctccac1020
ttggacaaca acaagttggc cagggtgccc tcagggctcc cagacctcaa gctcctccag1080
gtggtctatc tgcactccaa caacatcacc aaagtgggtg tcaacgactt ctgtcccatg1140
ggcttcgggg tgaagcgggc ctactacaac ggcatcagcc tcttcaacaa ccccgtgccc1200
tactgggagg tgcagccggc cactttccgc tgcgtcactg accgcctggc catccagttt1260
ggcaactaca aaaagtagag gcagctgcag ccaccgcggg gcctcagtgg gggtctctgg1320
ggaacacage cagacateet gatggggagg cagagecagg aagetaagee agggeecage1380
tgegtecaae ceageeece acetegggte cetgaceea getegatgee ceateacege1440
ctetecetgg cteceaaggg tgeaggtggg cgeaaggeee ggeeeceate acatgtteee1500
ttggcctcag agctgcccct gctctcccac cacagccacc cagaggcacc ccatgaagct1560
tttttctcgt tcactcccaa acccaagtgt ccaaggetcc agtcctagga gaacagtccc1620
tgggtcagca gccaggaggc ggtccataag aatggggaca gtgggctctg ccagggctgc1680
egeacetgte cagacacaca tgttetgtte etecteetea tgeattteea geettteaac1740
cctccccgac tctgcggctc ccctcagccc ccttgcaagt tcatggcctg tccctccaag1800
acceptate captageest tegaceagte etecettetg tretetett cecegteett1860
tecteagace titetegett etgagetigg tggeetgtte ecteeatete teegaacetg1980
gettegeetg tecettteae tecacaceet etggeettet geettgaget gggaetgett2040
tetgtetgte eggeetgeae ceageceetg eccacaaaae eecagggaca geggteteec2100
cagootgooc tgotcaggoo ttgoccocaa acctgtactg tocoggagga ggttgggagg2160
tggaggccca gcatcccgcg cagatgacac catcaaccgc cagagtccca gacaccggtt2220
ttectagaag cccctcaccc ccactggccc actggtggct aggtctcccc ttatccttct2280
ggtccagcgc aaggagggc tgcttctgag gtcggtggct gtctttccat taaagaaaca2340
ccgtgcaacg tgaaaaaaa aaaaaaa
```

## (2) INFORMATION ON SEQ ID NO. 154:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1314 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```
cacacacctg cacatactca tgcatgcaca tgtacacacg cagtcacaca tgcactcacg
cagttgcaca cacacgcatg ctcactccca cactgtgtgc actcaggtgg ctgtgttgga 120
cagttgggcc cagggctccc ctgctgtcct gtggggccgg catctgctct ccttcttct 180
ccccaggtac ttctactccc gaaggattga catcaccctg tcgtcagtca agtgcttcca 240
caagetggcc tetgcctatg gggccaggca getgcagggc tactgcgcaa gcctetttgc 300
catectecte ecceaggace cetegtteea gatgeceetg gacetgtatg cetatgeagt 360
ggccacaggg gacgcctgc tggagaagct ctgcctacag ttcctggcct ggaacttcga 420
ggccttgacg caggccgagg cctggcccag tgtccccaca gacctgctcc aactgctgct 480
gcccaggagc gacctggcgg tgcccagcga gctggcccta ctgaaggccg tggacacctg 540
gagetggggg gagegtgeet eccatgagga ggtggaggge ttggtggaga agateegett 600
coccatgatg ctccctgagg agetetttga getgeagtte aacetgtece tgtactggag 660
ccacgaggcc ctgttccaga agaagactct gcaggccctg gaattccaca ctgtgccctt 720
ccagttgctg gcccggtaca aaggcctgaa cctcaccgag gatacctaca agccccggat 780
ttacacctcg cccacctgga gtgcctttgt gacagacagt tcctggagtg cacggaagtc 840
acaactggtc tatcagtcca gacgggggcc tttggtcaaa tattcttctg attacttcca 900
agoccoctot gactacagat actaccocta coagtootto cagactocac aacaccocag 960
cttcctcttc caggacaaga gggtgtcctg gtccctggtc tacctcccca ccatccaqaq1020
ctgctggaac tacggcttct cctgctcctc ggacgagctc cctgtcctgg gcctcaccaa1080
gtctggcggc tcagatcgca ccattgccta cgaaaacaaa gccctgatgc tctgcgaaqq1140
gctcttcgtg gcagacgtca ccgatttcga gggctggaag gctgcgattc ccagtgccct1200
ggacaccaac agctcgaaga gaacctcctc cttcccctgc cccggcagag cttttcaaac1260
gggctttccg caacgggtca atccgcgcct ttctaacttg acaaacttct tcag
```

### (2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 965 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
  - ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

cctcccaaag gaactcccca atactagaac tcatcccaaa ccccttgcac ttcaacaaat 60 taacgaaccc attececaac ccacaatacc ccacceteca acaacetaaa acaacgaett120 catgeteceg tgeccaaaac geacagaeet teaacetgga eggeteeetg atetatgaaa180 qactcccatc gtcttgcagt cggtcttcac cagcgtgcgg cagaaaatcg agaaggagga240 tgacagtgaa qqcqaggaga gtgaggagga ggaagagggc gaggaggaag gctccqaatc300 cqaatctcqq tccqtcaaaq tqaaqatcaa gcttqqccqq aaqqaqaaqq cacaqqaccq360 qctqaaqqqc gqccgqcggc ggccqagccg agggtcccga gccaagccgg tcgtgaqtga420 cgatgacagt gaggaggaac aagaggagga ccgctcagga agtggcagcg aagaagactg480 ageccegaca ttecagtete gacceegage ecetegttee agagetgaga tggcatagge540 cttagcagta acgggtagca gcagatgtag tttcagactt ggagtaaaac tgtataaaca600 aaagaatett eeatatttat acagcagaga agetgtagga etgtttgtga etggeeetgt660 cctggcatca gtagcatctg taacagcatt aactgtctta aagagagaga gagagaattc720 cqaattgggg aacacacgat acctgttttt cttttccgtt gctggcagta ctgttgcgcc780 gcagtttgga gtcactgtag ttaagtgtgg atgcatgtgc gtcaccgtcc actcctccta840 ctgtatttta ttggadaggt cagactogoo gggggooogg cgagggtatg tcagtgtcac900 tggatgtcaa acagtaataa attaaaccaa caacaaaacg caaaaaaaaa aaaccaaggg960 cgaga

#### (2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3101 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```
ctcgcgccgg acacagggag cagcgagcac gcgtttcccg caacccgata ccatcggaca 60 ggatttctcc gcctcagccc aacgggagg gctagttgca catagtgatt tagatgaaag 120 agctattgaa gctttaaaag aattcaatga agacggtgca ttggcagttc ttcaacagtt 180 taaaggacagt gatctctct atgttcagaa caaaagtgcc tttttatgtg gagtcatgaa 240 gacttacagg cagagagaa aacaagggac caacaggacac acacttgatg tgaccactgg 360 acagaggaag tatggagca cacctccaga ttccgttat tcaggatga aacttgttc 420 tggcactgag atatttgtg gaaagatccc aagagatcta tttgaggatg aacttgttcc 480 attattgag aaagctggac ctatatgga tcttcgtcta atgatggatc cacctcagc 540 tctcaataga ggttatgcgt ttgtcacttt ttgtacaaaa gaagcagctc aggaggctgt 600 taaactgtat aataatcatg aaattcgttc tggaaaacat attggtgtct gcatctcagt 660 tgccaacaat aggctttttg tgggctctat tcctaagagt aaaaccaagg aacagattct 720
```

tgaagaattt agcaaagtaa cagagggtct tacagacgtc attttatacc accaaccgga 780 tgacaagaaa aaaaacagag gcttttgctt tcttgaatat gaagatcaca aaacagctgc 840 ccaggtaaaa gtgctgtttg tacgcaacct tgccaatact gtaacagaag agattttaga 900 aaaggcattt agtcagtttg ggaaactgga acgagtgaag aagttaaaag attatgcgtt 960 cattcatttt gatgagcgag atggtgctgt caaggctatg gaagaaatga atggcaaaga1020 cttggaggga gaaaatattg aaattgtttt tgccaagcca ccagatcaga aaaggaaaga1080 aagaaaagct cagaggcaag cagcaaaaaa tcaaatgtat gacgattact actattatgg1140 tecaceteat atgeceete caacaagagg tegaggegt ggaggtagag gtggttatgg1200 atatcctcca gattattatg gatatgaaga ttattatgat tattatggtt atgattacca1260 taactatcgt ggtggatatg aagatccata ctatggttat gaagattttc aagttggagc1320 tagaggaagg ggtggtagag gagcaagggg tgctgctcca tccagaggtc gtggggctgc1380 tecteceege ggtagageeg gttatteaca gagaggaggt cetggateag caagaggegt1440 tcgaggtgcg agaggaggtg cccaacaaca aagaggccgc gggcagggaa aaggggtcgal500 ggccggtcct gacctgttac aatgaagact gacttgctat gtgggattac accagaagct1560 tgcagtggag taatggtaag gaaatcaagc aaccttaaat atgtcggctg tataggagca1620 tattctattg cagaagacct tcctatgaag atcatggaat caaatacggg acattgaact1680 aatacttgga ctttgatatg aatttcttta acaattttct ctgcagtgca agttattaaa1740 ctaaagctac totattttca aaatgtgtto caacagaaat cottcataac tootagcatg1800 gtatcttaat aaagaataaa gttcttttaa aaatctgctc taagtagatt tttccccttt1860 tttaaattaa ggatcccaac agtggtattt tgaaatattc tcttgaattt gtgcatttaa1920 attitatige agiggiatag atgaatgeea cigatggiat cettaaatti tattietget1980 caccaaggtt aatcatgatt gtctatatct tttttatagt gatcactttt gaattgtgtt2040 cagatatgca gtttcaggtg taatcatcag agctggttag tcaggcattc cagatagtgg2100 ttcttttcag aaccttttta aaagggttgg ttaactacct cagtagcaga ggattgaact2160 ataccctgtc tgtactgtac atagaaaatc tttgtagata aaagcaaggc ttgttaaata2220 tgatatgagg gtaagatttt aatataccaa atgtaacatt cttagttgcc tttagtttca2280 gaggettgta agaetteete atgaecatea taacaggeet tgettttgte gtattttgtg2340 gctgaaaaag cagccttgct tcttcagata ttgtagttat ttggatgtat aatagtttag2400 caagatgtta cttttgtaag acatcagatg ttcaaaaaag tgcatccgaa cttgtactaa2460 atactgcagt gtccctttat aaaaagtcag actaaaactg acaattgtac agcgaagcct2520 gacatttgga tattttgaag ttttttcata aatcatagaa attagtatat ggctgtagtt2580 tagcttttta ggtaaaaggt atgtttcatt agtgcatttc ttcctgctga tcactgtaaa2640 catgtgaatc agctttccat ttcttatgca ggtcatgata acttgtagag tagagtacaa2700 tcatttgtgc tatgttttta attttctaaa gcaccttgat gacagtgagt gtccagtggt2760 gaagcatcct ctattgaacc accctcaaaa atttttttgc caagtcctaa gttgatagct2820 ccttccccaa agggatactg cagttatatc acatacccaa taggcaccac gatgaagatc2940 agagettata ettaattaag gttttataca caccagttee eeagtaaatg caaatttaac3000 aagaaaatca gacatgtcat atgttcaaaa tgctcatggc aaacaatcat tttgcattcc3060 tgcaaataaa attgttttat actgtaaaac aaaaaaaaa a

- (2) INFORMATION ON SEQ ID NO. 157:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 983 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

gggcgggag cggcggtcca gactggggag ggacgcgcac cggccaggag gcttcaagag 60 gagggeacta gggeeetgeg ageggegtet taaceggegg egetaggaet eegegggaaa120 cggcgggggc ggacgggcgg caccaggacc caggggaacc gcgacgggcg ggcggcgagc180 aggcccggga gccgggaggt gcgggcggcg gcgctggacc cgacgcggcg agagagccc240 cgagatgccg agcaagaaga agaagtacaa cgcgcggttc ccgccggcgc ggatcaagaa300 gatcatgcag acggacgaag agattgggaa ggtggcggcg gcggtgcctg tcatcatctc360 ccgggcgctc gagctcttcc tagagtcgct gttgaagaag gcctgccagg tgacccagtc420 geggaaegga aagaceatga ecacateeca eetgaageag tgeategage tggageagea480 gtttgacttc ttgaaggacc tggtggcatc tgttcccgac atgcaggggg acggggaaga540 caaccacatg gatggggaca agggcgcccg cagggccgga agccaggcag cqqcqqccqq600 aagaacggtg ggatgggaac gaaaagcaag gacaagaagc tgtccgggac agactcggag660 caggaggatg aatctgagga cacagatact gatggggaag aggagacatc acaaccccca720 coccaggoca gocaccocto tgoccacttt cagagoccco cgacaccott cotgoccttc780 gestetaste tgestttges escagegess cegggesset cagsacetga tgaagaggac840 gaagaagatt acgactocta gogcottotg coccocagac catagococt tttagttggt900 tttagttgct ctggggggag gagagaaggt agagctgttc ttaaatttat taaaaaaaaa960 aataaaaggg aaaaaaaaaa aaa 983

- (2) INFORMATION ON SEQ ID NO. 158:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 293 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

FIDSYRCFQP KQEGAFTCWS AVTGARHLNY GSRLDYTLGD RTLVIDTFQA SFLLPEVMGS 60 DHCPVGAVLS VSSVPAKQCP PLCTRFLPEF AGTQLKILRF LVPLEQSPVL EQSTLQHNNQ120 TRVQTCQNKA QVRSTRPQPS QVGSSRGQKN LKSYFQPSPS CPQASPDIEL PSLPLMSALM180 TPKTPEEKAV AKVVKGQAKT SEAKDEKELR TSFWKSVLAG PLRTPLCGGH REPCVMRTVK240 KPGPNLGRRF YMCARPRGPP TDPSSRCNSS SGAGPAEPME AWGHLAWSPL HMI 293

- (2) INFORMATION ON SEQ ID NO. 159:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 131 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

ETLREKQEAA QGRGAGLRSC AGVTMPDVPR PPLVQLGLLQ RKNCTGRRGQ WEDPGAWHTC 60 RSGGPSWVLA SSQYASHMAP CGPHRGVCAR APPAQTSRMR SVTPSHLWLL KSWPAPSPLW120 PLPSLLESSG S

- (2) INFORMATION ON SEQ ID NO. 160:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

KRRPKLGPGF FTVRITHGSL WPPQRGVRKG PASTDFQNEV RNSFSSLASE VLACPFTTLA60 TAFSSGVFGV MRALISGRLG SSMSGEAWGQ LGÈG 94

- (2) INFORMATION ON SEQ ID NO. 161:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 136 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

LHQLAAQRLY LRPVRVGAWA LSLPGERRAE ISNQWSALVT WIPEGREGST VSSAADCCSK 60 NVFSTSFESP SHGNPSTPTR DPTPAVSRIS STCTSRDPND SCTNEHYGSC SNCLSTHCVY120 GWKAFGRKKG SSRLKG

- (2) INFORMATION ON SEQ ID NO. 162:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 281 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

PGSQKVAKAV PFPQRRTAAV RMSFPPHLNR PPMGIPALPP GIPPPGFF PPPVPPGTPM 60
IPVPMSIMAP APTVLVPTVS MVGKHLGARK DHPGLKAKEN DENCGPTTTV FVGNISEKAS120
DMLIRQLLAK CGLVLSWKRV QGASGKLQAF GFCEYKEPES TLRALRLHD LQIGEKKLLV180
KVDAKTKAQL DEWKAKKAS NGNARPETVT NDDEEALDEE TKRRDQMIKG AIEVLIREYS240
SELNAPSQES DSHPQEEEG KEGGHFPQIS SGPTDPLSTH H 281

- (2) INFORMATION ON SEQ ID NO. 163:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 103 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

CSLVQESLGS LEVQVEEILE TAGVGSLVGV LGFPWEGDSN EVEKTFLLQQ SAAEETVLPS 60 RPSGIQVTSA LHWFEISARR SPGRLSAQAP TRTGRKYSRC AAS 103

- (2) INFORMATION ON SEQ ID NO. 164:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

NISLLDHPGL QSCLYFLFWI LFTNRERYIS AWKWPDVWKL DIWHFGLHSH GYYSHNKDGS 60 GNSFLDLDQP SRYLGIYYIL FCIFLVLWRD SLAIFGLPEY VFCVYSAPVK WFCLVCHNPH120 GCYMSIS

- (2) INFORMATION ON SEQ ID NO. 165:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 382 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

HEVLCCRMAP LQKAKVIRLI KISPEKPITL AVGDGANDVS MIQEAHVGIG IMGKEGRQAA 60 RNSDYAIARF KFLSKLLFVH GHFYYIRIAT LVQYFFYKNV CFITPQFLYQ FYCLFSQQTL120 YDSVYLTLYN ICFTSLPILI YSLLEQHVDP HVLQNKPTLY RDISKNRLLS IKTFLYWTIL180 GFSHAFIFFF GSYLLIGKDT SLLGNGQMFG NWTFGTLVFT VMVITVTIKM ALETHFWTW1240 NHLVTWGSII FYFVFSLFYG GILWPFLGSQ NMYFVFIQLL SSGSAWFAII LMVVTCLFLD300 IKKVFDRHL HPTSTEKAQM YSNTVALSDE FIALQPLSRA RNQLSKLSLL KQMQVSSAWT360 PCAVSRKEKQ RVHLLEECWN EL

- (2) INFORMATION ON SEQ ID NO. 166:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 85 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

QELNKHKIHI LGAQKWPENP SIKQGKYKIK YNRSPGNEMV DPSPKMSFQS HLYCDCNNHD60 CEDQSAKCPV SKHLAISKQR CIFPY

- (2) INFORMATION ON SEQ ID NO. 167:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 496 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

RLEKGPLPFQ MPGMRLPETQ VLPGEIDETP LSKPGHDLAS MEDKTEKWSS QPEGPLKLKA 60
SSTDMPSQIS VVNVDQLWED SVLTVKFPKL MVPRFSFPAP SSEDDVFIPT VREVQCPEAN120
IDTALCKESP GLWGASILKA GAGVPGEQPV DLNLPLEAPP ISKVRVHIQG AQVESQEVTI180
HSIVTPEFVD LSVPRTFSTQ IVRESEIPTS EIQTPSYGFS LLKVKIPEPH TQARVYTTMT240
QHSRTQEGTE EAPIQATPGV DSISGDLQPD TGEPFEMISS SVNVLGQQTL TFEVPSGHQL300
ADSCSDEEPA EILEFPPDDS QEATTPLADE GRAPKDKPES KKSGLLWFWL PNIGFSSSVD360
ETGVDSKNDV QRSAPIQTQP EARPEAELPK KQEKAGWFRF PKLGFSSSPT KKSKSTEDGA420
ELEEQKLQEE TITFFDARES FSPEEKEEGE LIGPVGTGLD SRVMVTSAAR TELILPEQDR480
KADDESKGSG LGPNEG

## (2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

SLPASMYWDS KHSHLKFLLA TSLQTAVQMR SQQKFLSFPL MIAKRQPHHW QMKAGLQKTN 60 QKVKNLVCSG FGFQTLGFPL LLMRQVLIPK MTSRDLLPFK HSLRHDQRQN CLKNRRRQAG120 SDFPN

- (2) INFORMATION ON SEQ ID NO. 169:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 130 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

MGADLWTSFL ESTPVSSTEE ENPMFGSQNQ SRPDFLLSGL SFGALPSSAS GVVASWLSSG 60 GNSRISAGSS SEQLSASWWP EGTSNVSVCC PSTLTLEEII SNGSPVSGWR SPEMESTPGV120 ACMGASSVPS 130

- (2) INFORMATION ON SEQ ID NO. 170:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

VVYRGVKCFI DKKKKTALEP TYSSSSSSS SSSSSSSS SSSSSSSS SSFFFLLFSA 60 LTTPFFAASG FPLARYAAIS FSYFSFTSQP SFHKAACHLQ QCYSTSLPVS SQHHQWTGQD120 VLL

- (2) INFORMATION ON SEQ ID NO. 171:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 157 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

KKLYLLRSIQ NVNKTAAIFF LQLQSGIQLT EQQLSSYKLH QRQLKMKKIK PKKKTKRKKK 60 KKQKTKLPSP YITNLCCAPT RTCFKFPCQF TTPILYQARL VAIENTTRTG LSKDTFGSVL120 TIQKKTLYSL KTNLTQPYIS IFFFKRSELC TGGLNAL

- (2) INFORMATION ON SEQ ID NO. 172:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 152 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

LNMGKGDPKK PRGKMSSYAF FVQTCREEHK KKHPDASVNF SEFSKKCSER WKTMSAKEKG 60 KFEDMAKADK ARYEREMKTY IPPKGETKKK FKDPNAPKRP PSAFFLFCSE YRPKIKGEHP120 GLSIGDVAKK LGEMWNNTAA DDKQPYEKKA AK

- (2) INFORMATION ON SEQ ID NO. 173:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 281 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

SGSAGPGPRG PRATESGKRM DCPALPPGWK KEEVIRKSGL SAGKSDVYYF SPSGKKFRSK 60
PQLARYLGNT VDLSSFDFRT GKMMPSKLQK NKQRLRNDPL NQNKGKPDLN TTLPIRQTAS120
IFKQPVTKVT NHPSNKVKSD PQRMNEQPRQ LFWEKRLQGL SASDVTEQII KTMELPKGLQ180
GVGPGSNDET LLSAVASALH TSSAPITGQV SAAVEKNPAV WLNTSQPLCK AFIVTDEDIR240
KQEERVQQVR KKLEEALMAD ILSRAADTEE MDIEMDSGDE A

- (2) INFORMATION ON SEQ ID NO. 174:
  - (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 102 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

IIDIYIKNTS KKALVSAIKK LYVLGYIFFL TGKSQWKHFC SISRNFLLGK VGRKLPDHIL 60 RLHLHCPFQY PSLLYQQLAT RCLPSVLLPI SCVLAVLALP VS 102

- (2) INFORMATION ON SEQ ID NO. 175:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

IYTSKIHLKR HWLVLLKSSM CSGTFFFLQA KASGNIFVQF LGIFSWGKSV ESYLIIFLGF 60

ISTVHFNIHL FCISSSRQDV CHQCFFQFLA YLLYSLFLFP DVFICDNKSF AEGLRCVKPN120 SRVLFHSSGD LPCDWRRACV QSTGNSR 147

- (2) INFORMATION ON SEQ ID NO. 176:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 85 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

ECPLGARGPW EPRHPFPLGR GARSRHPCTH GRLAPPQSPP HSQQPFHSHC PSRSPQPSLR60 PHPHPLRAQG CNPSLSTTHR WYSWG 85

- (2) INFORMATION ON SEQ ID NO. 177:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 128 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

NALWGPGAPG SPATLSHLAG VPAAATPARM AGWHPPRALP TASSLSTVTA LPAVPSLPYG 60 LTRTPSEPRA ATPHYPPRTD GTAGAEQPHV EPERVPGARG QDAGGRMTAC PCLTSWGTTL120 DRGIGQDP 128

- (2) INFORMATION ON SEQ ID NO. 178:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

MPFGGQGPLG APPPFPTWPG CPQPPPLHAW QAGTPPEPSP QPAAFPQSLP FPQSPAFPTA 60 SPAPPQSPGL QPLIIHHAQM VQLGLNNHMW NQRGSQAPED KTQEAE 106

- (2) INFORMATION ON SEQ ID NO. 179:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 77 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GNPELPWRKF QCQHSCSLWP SPTLWPEIPQ SNLEPKRTQR TLDPNCPRPS PEVGVTNSSG60 LRHMKKLYIN PRQATNP 77

- (2) INFORMATION ON SEQ ID NO. 180:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 64 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

PPTHTRQVGE EIQSCHGENS SVSILAPCGP LLHSGQRYHS QTWSQKGHKG LSTQTAPDPL60 QRLG

- (2) INFORMATION ON SEQ ID NO. 181:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 206 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

RLSCAGTLSG SGPHPSRRLT QGRWVRKSRV AMEKIPVSAF LLLVALSYTL ARDTTVKPGA 60 KKDTKDSRPK LPQTLSRGWG DQLIWTQTYE EALYKSKTSN KPLMIIHHLD ECPHSQALKK120 VFAENKEIQK LAEQFVLLNL VYETTDKHLS PDGQYVPRIM FVDPSLTVRA DITGRYSNRL180 YAYEPADTAL LLDNMKKALK LLKTEL 206

- (2) INFORMATION ON SEQ ID NO. 182:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 206 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

RVFQEEELVR RQRNGASGPR PGLRRLRGGR RAVRRKERLL HRQLPAVHKR GARVKLSSPE 60 RDVERDVFLY RAYLAQRKFG VVLDEIKPSS APELQAVRMF ADYLAHESRR DSIVAELDRE120 MSRSVDVTNT TFLLMAASIY LHDQNPDAAL RALHQGDSLE CTAMTVQILL KLDRLDLARK180 ELKRMQDLDE DATLTQLKVL VSLQRV

- (2) INFORMATION ON SEQ ID NO. 183:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 111 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

  LPRPRESEGQ HRGRAGPRDE QERGRDQHHL PAHGRLHLSP RPEPGCRPAC AAPGGQPGVH 60
  SHDSADPAEA GPPGPRPEGA EENAGPGRGC HPHPAQGLGK LATGVKAQGS F 111
  - (2) INFORMATION ON SEQ ID NO. 184:
    - (i) SEQUENCE CHARACTERISTIC:
      - (A) LENGTH: 165 amino acids
      - (B) TYPE: Protein
      - (C) STRAND: individual
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

GTILPIPEIR RILELLHPLQ AYQDLELGEG GILVQVLHSL QLLPGEVQAV QLQQDLHCHG 60 CALQAVPLVQ RTQGGIRVLV VEIDGGGHEQ EGGVGHVHAP AHLSVQLGHD AVPPTLVGEV120 VSKHAHGLEL RGRGGLDLIQ DHTELPLRQV RSIQEDVPLH VSLWA 165

- (2) INFORMATION ON SEQ ID NO. 185:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

LLSMRMILKP QSFMILMMLR SSNRVTWKLL LIGLDYIRYQ MENQKTSLLL MENSKTRLLL60 LKLLNPLINV GKHCL

- (2) INFORMATION ON SEQ ID NO. 186:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 340 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

RTVIDAMSAL LRLLRTGAPA AACLRLGTSA GTGSRRAMAL YHTEERGQPC SQNYRLFFKN 60 VTGHYISPFH DIPLKVNSKE ENGIPMKKAR NDEYENLFNM IVEIPRWTNA KMEIATKEPM120 NPIKQYVKDG KLRYVANIFP YKGYIWNYGT LPQTWEDPHE KDKSTNCFGD NDPIDVCEIG180 SKILSCGEVI HVKILGILAL IDEGETDWKL IAINANDPEA SKFHDIDDVK KFKPGYLEAT240 LNWFRLYKVP DGKPENQFAF NGEFKNKAFA LEVIKSTHQC WKALLMKKCN GGAINCTNVQ300 ISDSPFRCTQ EEARSLVESV SSSPNKESNE EEQVWHFLGK

- (2) INFORMATION ON SEQ ID NO. 187:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 131 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

LSILYILFNG IHWLLGGNLH FSICPPRYFY NHIKQILIFI ISCFLHRNAI FLFRVHLQRN 60 IMKGGNVVTS YILKEEAVIL RAGLAALLSV VQGHSTARPG PCTGPQPQAR SGWGTRAQQP120 QQRAHGVNDG P

- (2) INFORMATION ON SEQ ID NO. 188:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 436 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

GRGMGRVQLF EISLSHGRVV YSPGEPLAGT VRVRLGAPLP FRAIRVTCIG SCGVSNKAND 60
TAWVVEEGYF NSSLSLADKG SLPAGEHSFP FQFLLPATAP TSFEGPFGKI VHQVRAAIHT120
PRFSKDHKCS LVFYILSPLN LNSIPDIEQP NVASATKKFS YKLVKTGSVV LTASTDLRGY180
VVGQALQLHA DVENQSGKDT SPVVASLLQK VSYKAKRWIH DVRTIAEVEG AGVKAWRRAQ240
WHEQILVPAL PQSALPGCSL IHIDYYLQVS LKAPEATVTL PVFIGNIAVN HAPVSPRPGL300
GLPPGAPPLV VPSAPPQEEA EAEAAAGGPH FLDPVFLSTK SHSQRQPLLA TLSSVPGAPE360
PCPQDGSPAS HPLHPPLCIS TGATVPYFAE GSGGPVPTTS TLILPPEYSS WGYPYEAPPS420
YEQSCGGVEP SLTPES

- (2) INFORMATION ON SEQ ID NO. 189:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

SVLFTGVVSP GPSSLPPPPQ PQGEEGGCRG AGRGWAGPEW ARLGQERRHE ALGAPVPGQR 60 PGLPGEGSTG SALRGQAGFH AAAALLIRRW GLIGVAPRTV LWRKNQGAGS GHWPPGALCK120 VGDSGTC

- (2) INFORMATION ON SEQ ID NO. 190:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 213 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

LVLNVGMQLQ CLPHHIAAEI SAGCEDHAAR LHQLVGELLG GRGHVGLLNV WDAVQVQGAQ 60 DIEHEAALVI LGKPWRVDGG PHLVHDLPER TLKGRGCSGR KQELEGEAVL SSGQAPLVCQ120 RQGTVEVTLL HYPRCVISLV GDPAGTYAGH PDGSERQRCP QAHAHGPSQR LPGAVDDAAV180 AQADLEELHS PHAAASPASR AATPPPAARE SRL 213

- (2) INFORMATION ON SEQ ID NO. 191:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 635 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

GGVSPWRACV QQRMEESEPE RKRARTDEVP AGGSRSEAED EDDEDYVPYV PLRQRRQLLL 60
QKLLQRRKG AAEEEQQDSG SEPRGDEDDI PLGPQSNVSL LDQHQHLKEK AEARKESAKE120
KQLKEEEKIL ESVAEGRALM SVKEMAKGIT YDDPIKTSWT PPRYVLSMSE ERHERVRKKY180
HILVEGDGIP PPIKSFKEMK FPAAILRGLK KKGIHHPTPI QIQGIPTILS GRDMIGIAFT240
GSGKTLVFTL PVIMFCLEQE KRLPFSKREG PYGLIICPSR ELARQTHGIL EYYCRLLQED300
SSPLLRCALC IGGMSVKEQM ETIRHGVHMM VATPGRLMDL LQKKMVSLDI CRYLALDEAD360
RMIDMGFEGD IRTIFSYFKG QRQTLLFSAT MPKKIQNFAK SALVKPVTIN VGRAGAASLD420
VIQEVEYVKE EAKMVYLLEC LQKTPPPVLI FAEKKADVDA IHEYLLLKGV EAVAIHGGKD480
QEERTKAIEA FREGKKDVLV ATDVASKGLD FPAIQHVINY DMPEEIENYV HRIGRTGRSG540
NTGIATTFIN KACDESVLMD LKALLLEAKQ KVPPVLQVLH CGDESMLDIG GERGCAFCGG600
LGHRITDCPK LEAMQTKQVS NIGRKDYLAH SSMDF

- (2) INFORMATION ON SEQ ID NO. 192:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

KPSRRCRPCC RCCIAGMSPC WTLEESAAVP SAGAWVIGSL TAPNSRLCRP SRSATSVART 60
TWPTAPWTSE PTVFPSLQEA SVPKTATSLH IQQPPGQNQH FSSAGLEWAR LVLAACSLCS120
SELLFLFPFT PAAIKAQTSS PKKKKKK

- (2) INFORMATION ON SEQ ID NO. 193:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 150 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

DILLALPECL DGLSPFLLVF APMDGYGLNP LEQQVLVDGV HVCLLLCKDE YRRGCLLQAL 60 EQVHHLGLLL HIFYLLDDIQ AGSPSAPHID GHRLYKGTLS KVLNLLRHGG TEEQGLSLAL120 EVGEDGTDVT LEAHVDHAVS LVQGQVATDV

- (2) INFORMATION ON SEQ ID NO. 194:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 310 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

EAPAAARTQS PAAAAQRGDN VYVVTEVLQT QKEVEVTRTH KREGSGRFSL PGATCLQGEG 60 QGHLSQKKTV TIPSGSTLAF RVAQLVIDSD LDVLLFPDKK QRTFQPPATG HKRSTSEGAW120 PQLPSGLSMM RCLHNFLTDG VPAEGAFTED FQGLRAEVET ISKELELLDR ELCQLLLEGL180 EGVLRDQLAL RALEEALEQG QSLGPVEPLD GPAGAVLECL VLSSGMLVPE LAIPVVYLLG240 ALTMLSETQH KLLAEALESQ TLLGPLELVG SLLEQSAPWQ ERRPCPCPPG SWGTAGAKEH300 RPGSCWTSVA

- (2) INFORMATION ON SEQ ID NO. 195:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 244 amino acids

    - (B) TYPE: Protein (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

TTGIASSGTS IPEDNTRHSR TAPAGPSRGS TGPRLWPCSS ASSKARRASW SRSTPSRPSS 60 SSWHSSLSKS SSSLEMVSTS ARRPWKSSVN APSAGTPSVR KLWRHLIMER PEGSCGQAPS120 LVERLWPVAG GWKVLCFLSG KRRTSKSESI TSWATRNARV LPEGMVTVFF WLRWPWPSPC180 KHVAPGRENR PEPSRLWVRV TSTSFCVCST SVTTYTLSPR CAAAAGLCVL AAAGASHGAE240 244

- (2) INFORMATION ON SEQ ID NO. 196:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 229 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TGHMATGLLA FLGLAAGGQT LCPAGELPGH ARAQASGAPG SVLIAVPGRR RVHTCGPGPA 60
APSTRGECPP PALGHTRPAR PRPVLLRPSC SPGARGAGTW SALLPRGTLL QEAAHQLERP120
QQGLRLQRLR QQLVLRFTQH GQCPQQVDNR DSEFRHQHSG GQHQALQDST CWTVQGLHRP180
KALALLQRLL QGSQGQLVPQ HPLQALQQQL AQLSVQKLQF LGDGLHLCP 229

- (2) INFORMATION ON SEQ ID NO. 197:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TEILPVFVRL AGVPICSTGN ASAMLQPQKP GLSLQQQAEP CLWSGAVHSS VCLVLGLELD60 RGGVSSPSLN SEQTLCLAPV CPGNSPGPHW EPLVF

- (2) INFORMATION ON SEQ ID NO. 198:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

AVPRGSLRED GKVRCMSNLL MAGSPLCPLS LALVIAELCA QCCGLAVARL FLWGARAGCG 60 NQSSQTDVSQ AEDSFLAEVS PHLQVSGWGG ARRGRHTPCL T 10.1

- (2) INFORMATION ON SEQ ID NO. 199:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 155 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

VRHTSHLAVL TQGAPGHCSC AAWALLRTP RAPNEGLGNC LGTLGPGTGS VLNSGKVKRP 60 HLYPAQAQEQ GRQSCGQHPT TDTVLPAAGV RGLVSEAAAW HWHCLCYRWG LLRVSQIQGE120 FQFTQPKGPV CRAALTRAQQ HSTELGKGRG ERVKD 155

- (2) INFORMATION ON SEQ ID NO. 200:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 138 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

RMKCSQPPRC HFQSDFQKCA PCPRAQTHWL EPPGRVQTIS SMRNAQKGFA DSIRLWRLPA 60 SGVGWVVSPP IQTQEVAPEG MYLVGSSSGT LGGCRALTQV FLSLSSLGCV CACACACLCF120 SLWAHQDAPR RACARVPT 138

- (2) INFORMATION ON SEQ ID NO. 201:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 132 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

VHGREARLGT LAGTAALKPA LLSGYQTFKG QDVLRRVPVA ARRPAGACPR VTAWRCWGSG 60 HLPCLECQEG EAFEEASVLA ARSLSQPLPG SCTGQGLIPC HAGPLEQVGW GWYVLSPQPW120 QPCPLGKVIS DL 132

- (2) INFORMATION ON SEQ ID NO. 202:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 131 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

RLFIGCSLQN KQRWDWGPSL GPCTPLSRAY NHVHRPGRGP ALCPTKSSLH QSSWSPPLRD 60 PAQLPRSWGI GTRVPWRVQE MRRIPCTLRR TPTPELWSRG HCERRQRERH VEDTLTDPVG120 SGRAEDRHTK P

- (2) INFORMATION ON SEQ ID NO. 203:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 76 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

  LAAIKDQLEG VQQALSQAAP IPEEDTDTEE GDDFELLDQS ELDQIESELG LTQDQEAEAQ60
  QNKKSSGFLS NLLGGH
  76
  - (2) INFORMATION ON SEQ ID NO. 204:
    - (i) SEQUENCE CHARACTERISTIC:
      - (A) LENGTH: 102 amino acids
      - (B) TYPE: Protein
      - (C) STRAND: individual
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

RVCSKHFLRL PPSQKRTQTL KKVMTLNYLT SQSWIKLRVN WDLHKTRKQK HSKIRSLQVS 60 FOICWEAINL GISLQQSTKN TKKISNKKKK KKRKRKKLNC KL 102

- (2) INFORMATION ON SEO ID NO. 205:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

ICLHHNHCLC DTQLLAFYGL IPPTARLEMA VNGACFFTNK PKSTTAEITW KRFSLSRVLK60 YTFKFFPKKL ILIVFPKSFN 80

- (2) INFORMATION ON SEQ ID NO. 206:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 76 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

GKPAALEAHQ GSRLQGRSRE QAAIPPLLSS RTQLCGLGFL FAGLAPCRTL VLELEGPILP60 RGDSQGCRGI GWRRVL 76

- (2) INFORMATION ON SEQ ID NO. 207:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 72 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

NLRVSQLPWK PTRAPDCREE AGSRQPYLHS CPQGLSCVAL DFFLRDLRPA GHWCWSWRVL60 SCPGVTPRVA GG

- (2) INFORMATION ON SEQ ID NO. 208:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 73 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

  PGMSSLQDRH GRTIWFQVGP YCSHRQRPQE ADGWKRGVTI TGVVMLRVCL DPPRTTLFLR60

  VTPLPSHASQ GCS

  73
- (2) INFORMATION ON SEQ ID NO. 209:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 182 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

QRWLWTSSTS PCWIRAFLPP AGQVWPCSLG RAPAPLTTLQ LTMQLMPKLW CPVCSSPGSH 60 CHLQRGSLLR PTLLHLAPPW LLAWPNLAFC AMLELELLLF FRGGNRVESG KGLAPKCCCC120 GFFAFSKDAL PGPKLQTAVL SKQVRSLGFG AHLLSGSISI LLLATSGQRP PQPHIARCWQ180 KG

- (2) INFORMATION ON SEQ ID NO. 210:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 130 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

VGPGKQPWWG QVKQCGSQQG TPLKVAVAPR AAAHWTPQLW HQLHGELQSG QRGWGPAKRA 60 RPDLPSGRQE GPDPARRSRG SPQPPLLLIA TGTSGDRLCS WESRSPGFVG LPAGDRHVSH120 RERPGSRPQL 130

- (2) INFORMATION ON SEQ ID NO. 211:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 111 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

VTGKGRDPGL SCSSSWKRWS RTVTIHADTE QQYETEQLRA VSSSAEAAWA ATPPFCNHPM 60 MSPPHLTSRW GWMAEQMKPA LWRGSLTEMH TFMGEVDGHL TSLMFHTVDC T 111

- (2) INFORMATION ON SEQ ID NO. 212:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 243 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

DVQVAGPEPD CRVHSHVLPG QAHRLAPGPY SVGESLQPRE GCEDCDRQKA NLRIRFKPSL 60 FQHVGTHSSL AGKIQKLKDK DFGKQALRKE HVNPPAEVST SLKTYQHFTL EKAYLREDFF120 WAFTPAAGDF IRFRFFQPLR LERFFFRSGN IEHPEDKLFN TSVEVLPFDN PQSDKEALQE180 GRTATLRYPR SPDGYLQIGS FYKGVAEGEV DPAFGPLEAL RLSIQTDSPV WVILSEIFLK240 KAD

- (2) INFORMATION ON SEQ ID NO. 213:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 244 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

GRTGVSVVMG IPSVRREVHS YLTDTLHSLI SELSPQEKED SVIVVLIAET DSQYTSAVTE 60
NIKALFPTEI HSGLLEVISP SPHFYPDFSR LRESFGDPKE RVRWRTKQNL DYCFLMMYAQ120
SKGIYYVQLE DDIVAKPNYL STMKNFALQQ PSEDWMILEF SQLGFIGKMF KSLDLSLIVE180
FILMFYRDKP IDWLLDHILW VKVCNPEKDA KTVTGRKPTC GSASNRPSSS TWALTPRWLA240
RSRN

- (2) INFORMATION ON SEQ ID NO. 214:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 210 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

PAESQPADPL QTVPLPARGH SLLAGWQDPE TEGQRLWKAG AAEGACEPAS RGEHEPEDIP 60 ALHPGESLPA RGLLLGLHPC RGGLHPLPLL PTSKTGAVLL PQWEHRAPGG QALQHVCGGA120 ALRQPSVRQG GPAGGPHRHP PVPSEPRRLP PDRLLLQGSG RGRGGPSLRP SGSTAPLDPD180 GLPCVGDSER DLPEKGRLSC GLLRVPCGQP 210

- (2) INFORMATION ON SEQ ID NO. 215:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 128 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

GGAGLVHGSA DWPCLAPWRV SSCFLPGTEL RGLGAPGAKS RLWCRGGGLS LNRHPEVLLR 60 CWVHPEWHGE QLWPVLLPRP VLGKLSSGPS LQRPRMGWVW GTHGEWPEEL RVKRAPVCWL120 QRPGAPLS

- (2) INFORMATION ON SEQ ID NO. 216:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

FPQDWPRKEH RPQLLPVPLR VDPASQEHLR VSVKRQASTP APEPALSSRC PQTPQLCARQ 60 EAARHTPGRQ ARPVRGPMDK PSPASGKTGP FPTGHAPELW QIAGAIVWGE FNKSPFENEK120 KKKK

- (2) INFORMATION ON SEQ ID NO. 217:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 142 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

VPHTHPILGL CKEGPELSFP RTGLGRSTGH SCSPCHSGWT QHLRSTSGCR LRDRPPPLHQ 60 SLLLAPGAPR PRSSVPGKKQ LDTRQGAKHG QSADPWTSPA PPQGKQGLSL QDTPQSCGRL120 QEPSCGENLI KALLKMKKKK KK 142

- (2) INFORMATION ON SEQ ID NO. 218:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 379 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

RRGLEGFNGG WTEMPGILWM EPTQPPDFAL AYRPSFPEDR EPQIPYPEPT WPPPLSAPRV 60
PYHSSVLSVT RPVVVSATHP TLPSAHQPPV IPATHPALSR DHQIPVIAAN YPDLPSAYQP120
GILSVSHSAQ PPAHQPPMIS TKYPELFPAH QSPMFPDTRV AGTQTTTHLP GIPPNHAPLV180
TTLGAQRPPQ APDALVLRTQ ATQLPIIPTA QPSLTTTSRS PVSPAHQISV PAATQPAALP240
TLLPSQSPTN QTSPISPTHP HSKAPQIPRE DGPSPKLALW LPSPAPTAAP TALGEAGLAE300
HSQRDDRWLL VALLVPTCVF LVVLLALGIV YCTRCGPHAP NKRITDCYRW VIHAGSKSPT360
EPMPPRGSLT GVQTCRTSV

- (2) INFORMATION ON SEQ ID NO. 219:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 157 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

VDTDECQIAG VCQQMCVNYV GGFECYCSEG HELEADGISC SPAGAMGAQG SQDLGDELLD 60 DGEDEEDEDE AWKASTVAGR RCLGSCGWSL RSRLTLPWPI DRASQRTESH RYPTRSPPGH120 PRSVPPGSPT TPQCSPSPGL WWSLPRIPHC LLPTSLL 157

- (2) INFORMATION ON SEQ ID NO. 220:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 211 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

PPPPGPLCLL PIKSLCLLPP SPQPSPPSCP LRAPLTRPHP SALHIPIPKP PKSQGKMAPV 60
PSWPCGCPHQ LPQQPQQPWG RLVLPSTARG MTGGCWWHSW CQRVSFWWSC LHWASCTAPA120
VAPMHPTSAS LTAIAGSSML GARAQQNPCP PGAASQGCRP AEPACDGVQT PLMEYGALDT180
WPGLHQGPMG AAQLDRWLPA PQAQPGSSLN H

- (2) INFORMATION ON SEQ ID NO. 221:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

LGEPQISGAQ PGRVWGQLCQ STSQAHPLPG MPWDHGQGRL WGSETPLLST PSQNTLRVSG 60 LWREWGGRKN WHLPREGDER FALILREASE KCFKCVCMRQ AVGSGGLSSP LPPSFPK 117

- (2) INFORMATION ON SEQ ID NO. 222:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 198 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

NKELSSLKSS DVVMTHTESC ITVASRATHL FGLSDGHSFT TQQQTPHTGT RMSASTWEAV 60 AEPGRWPGPD HGLSGAGHQG VRVPMLPQGV GMTGRSLVTR QWTSLGEGWR ERAGQAPAAH120 RLAHANTLKA LLGGFSENQG EALVSFPRKV PILPPAPLSP EPRDPQGVLA GGAKQRCLRP180 PEPSLPMIPR HARQGVGL

- (2) INFORMATION ON SEQ ID NO. 223:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 98 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

SHGMPGRGWA CEVDWHSCPH TLPGWAPEIW GSPSQHGVLG ACPGPFTRTE APHPLSHFSR60 WKTQRRKRPW GGVPSCLQLA PWVPLCGGSP DSISSASE 98

- (2) INFORMATION ON SEQ ID NO. 224:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 298 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

ATRRRAAEAG MAAVLQRVER LSNRVVRVLG CNPGPMTLQG TNTYLVGTGP RRILIDTGEP 60
AIPEYISCLK QALTEFNTAI QEIVVTHWHR DHSGGIGDIC KSINNDTTYC IKKLPRNPQR120
EEIIGNGEQQ YVYLKDGDVI KTEGATLRVL YTPGHTDDHM ALLLEEENAI FSGDCILGEG180
TTVFEDLYDY MNSLKELLKI KADIIYPGHG PVIHNAEAKI QQYISHRNIR EQQILTLFRE240
NFEKSFTVME LVKIIYKNTP ENLHEMAKHN LLLHLKKLEK EGKIFSNTDP DKKWKAHL 298

- (2) INFORMATION ON SEQ ID NO. 225:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 58 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GFSWGRSPLG RCWCLGGSWD PGYSPTHARL DWTAARRAAV QQPFPPQPPA GVSPIWIL 58

- (2) INFORMATION ON SEQ ID NO. 226:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 73 amino acids
    - (B) TYPE: Protein
      - (C) STRAND: individual
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

SGSLSLNHIS IFQINILLLS ISYNFFSLRI PWEFFNAIGS VIIDAFTNIS YASRMISVPV60 SHYNFLDCCV KFS 73

- (2) INFORMATION ON SEQ ID NO. 227:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 141 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

AFLLRPSVTA STRLLPVCAS PRSSPGPSPA QQQQAWQQAW SSARAPSRCR ARPSSSERPC 60 PAVGRLASLY CCCMVFASPP RPGRTWVHCT GWPRLATGLW PLTCQVWGTP RKQQPLPLLG120 SWPLAASWRL WWMPWSWAPR L

- (2) INFORMATION ON SEQ ID NO. 228:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 244 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

VPPPALGHRQ HAPASRLRES TQLPRPFTST AAAGMAASVE QREGTIQVQG QALFFREALP 60 GSGQARFSVL LLHGIRFSSE TWQNLGTLHR LAQAGYRAVA IDLPGLGHSK EAAAPAPIGE120 LAPGSFLAAV VDALELGPPV VISPSLSGMY SLPFLTAPGS QLPGFVPVAP ICTDKINAAN180 YASVKTPALI VYGDQDPMGQ TSFEHLKQLP NHRVLIMKGA GHPCYLDKPE EWHTGLLDFL240 QGLQ 244

- (2) INFORMATION ON SEQ ID NO. 229:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 144 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

WTDHNRGAQL QGIHHSRQEA ARGQLPNRGR GCCFLGVPQT WQVNGHSPVA SLGQPVQCTQ 60 VLPGLGGEAN TMQQQYREAS LPTAGQGLSE EEGLALHLDG ALALLHACCH ACCCCAGEGP120 GELRGLAQTG SRRVLAVTEG RRRN

- (2) INFORMATION ON SEQ ID NO. 230:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 135 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

LEFFIPCLGS VNEACLFPGV SFHGLYFSSS SGSFAGSSLW KLHERWLGLG FAGVYSRVKA 60 EWDLRPRLGT TQAEKGRFHH SQCPPHSTTS ARAPPSLLPH PAIVRGATVG RRVPRRGLFL120 135 LPVPEKAFPL LKFKH

- (2) INFORMATION ON SEQ ID NO. 231:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 96 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GGPVCWEPQV TPFSSYSVPG ASCPPLQILG KENVYVAGYC MVTSEGRPLG THLPTAAQAR60 AQAHLLVLRP QIKPSPHHMA SDRFLPSRKF CGCAVL

- (2) INFORMATION ON SEQ ID NO. 232:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 83 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CCGEGTVNDG NVPSQPGSCL TWVSNPTLPS PWSTLQRSRG PANAREVSTE KSLQNSHWKR60 RNKGHGKKPQ GRDRPRSQTL GRE

- (2) INFORMATION ON SEQ ID NO. 233:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 52 amino acids

    - (B) TYPE: Protein (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

- (2) INFORMATION ON SEQ ID NO. 234:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

LGSAWQQLRR PEASETLRLV GTHRPRQRAL PRQRVASPPP RRGLGLTSPP VRLGQVVPGL60 MPGVVSAAGT QVRRLDEVPA SLRLQHHLQL REGL 94

- (2) INFORMATION ON SEQ ID NO. 235:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

ARPSRSWRWC CSRSDAGTSS RRRTWVPAAL TTPGIRPGTT CPRRTGGEVR PSPRRGGGLA60 TRCLGKARWR GLCVPTSRRV SDASGRRSCC QAEPR 95

- (2) INFORMATION ON SEQ ID NO. 236:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 174 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

APTNTRSSK FATSGSPGYP IASSGASPEV RQRRTTFFRF RPGESLCGDM KLLTHNLLSS 60 HVRGVGSRGF PLRLQATEVR ICPVEFNPNF VARMIPKVEW SAFLEAADNL RLIQVPKGPV120 EGYEENEEFL RTMHHLLLEV EVIEGTLQCP ESGRMFPISR GIPNMLLSEE ETES 174

- (2) INFORMATION ON SEQ ID NO. 237:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 225 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

YRAQKHCVWC HWVKGWGYTR QNSETGYRST KIHSHNKKNW RLAQSTLSFL FTQQHVGDPA 60 ADGEHTSRFR ALQGALYHFH LQQQVVHGPQ KLLILLISLN RPFRHLDQTQ VIGRLQERRP120 LHFRYHTRHE VGVEFHRADT DLGGLEAQGE ATGPHPPHMR AQQIVGKQFH VAAQTLARPE180 PEKGRPPLPH FRGCSTRCYW IARRTGSGEL AGTSRVCGSS FLYAN 225

- (2) INFORMATION ON SEQ ID NO. 238:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 209 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

TFNEKKIYNT ELKNTVFGVI GSRVGDTHGR IRKQGIDQQK YTVITRKTGA WHNQLSVSSS 60 LSSMLGIPRL MGNIRPDSGH CRVPSITSTS SSRWCMVLRN SSFSSYPSTG PFGTWIRRKL120 SAASRNADHS TLGIIRATKL GLNSTGQIRT SVAWRRRGKP RDPTPRTCEL SRLWVSSFMS180 PHKLSPGRNR KKVVLRCLTS GDAPLDAIG 209

- (2) INFORMATION ON SEQ ID NO. 239:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 146 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

INAFSHRNAK ININPPDAVA AALRPKSQRP RLTIIKVFSE SVGVSVNGCA LGGTVERCAK 60 SELQTIGQGH GVATRRLSA GAPPRTHSQQ SSHWEELKNK HLQGRGKRPR SRRSRARASA120 ARGAPTGSQR GGSPKRARSG RSRVLA

- (2) INFORMATION ON SEQ ID NO. 240:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 134 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

SRTFSFLSFL HCANILTLFV SFQEPHRHIQ VKRSLNKCLQ PSQCKNKYQS SRRSSSRAAP 60. KVPTATPNNY KSVQRECWRE CEWVCAGGHG GAVCKIGVAN HRTRAWSGYP PPTQRGRASP120 HTLTAEFALG RVKK

- (2) INFORMATION ON SEQ ID NO. 241:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

PARTRORPLL ARFGLPPRCE PVGAPLAALA LARERRERGR FPRPCKCLFF NSSQCELCCE 60 CVRGGAPALS RRRVATPCPC PMVCNSDFAH RSTVPPSAHP FTLTPTLSLN TFIIVRRGRW120 DFGRSAAATA SGGLIFIFAL RWLKAFI

- (2) INFORMATION ON SEQ ID NO. 242:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 88 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

PVLCRGNSGS LSRKFPPKPQ KPADKDHPRT CVYLENRSPG KSDLSATPGR SGLESGYQNL60 LRQHQPHGRC PTWPGSRWKV PRRFPGYG 88

- (2) INFORMATION ON SEQ ID NO. 243:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 164 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

QDGCPDSGDF AALQSLLKAS SKDVVRQLCQ ESFSSSALGL KKLLDVTCSS LSVTQEEAEE 60° - LLQALHRLTR LVAFRDLSSA EAILALFPEN FHQNLKNLLT KIILEHVSTW RTEAQANQIS120 LPRLVDLDWR VDIKTSSDSI SRMAVAPPGL VPDGRFQGGS QAMG 164

- (2) INFORMATION ON SEQ ID NO. 244:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 87 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

FAWASVLQVD TCSRMIFVSR FLRFWWKFSG KRARIASAED RSRNATSLVR RCRAWSSSSA60 SSWVTDKLEH VTSKSFFKPR AELEKLS 87

- (2) INFORMATION ON SEQ ID NO. 245:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 129 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

DGPGGPTAHP HRCAHPPGVC PGQAPAHLLL CAAAPGHPGQ GQQPAAGGLV GDADRAGDLE 60 CSPRRIFLHP RLHPPRHLGS CHLDRGCGCA GWSCCLHLRE TGWYILGPAE DSASAGSFLH120 SHRCPQTLE 129

- (2) INFORMATION ON SEQ ID NO. 246:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 268 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
   (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

ASPSNSQPTS PASAPALPPP ARRSRGAQTV SLTMGTADSD EMAPEAPQHT HIDVHIHQES 60 ALAKLLLTCC SALRPRATQA RGSSRLLVAS WVMQIVLGIL SAVLGGFFYI RDYTLLVTSG120 AAIWTGAVAV LAGAAAFIYE KRGGTYWALL RTLLALAAFS TAIAALKLWN EDFRYGYSYY180 NSACRISSSS DWNTPAPTQS PEEVRRLHLC TSFMDMLKAL FRTLQAMLLG VWILLLLASL240 APLWLYCWRM FPTKGKRDQK EMLEVSGI 268

- (2) INFORMATION ON SEQ ID NO. 247:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 103 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

DCTQDPQHDL HHPRGHQQPA AAPGLGGPGP QRRAAGEQEL GQGRLLVDVH IDVGVLWGLR 60°GHLITVGCSH CQGHSLRSSG PASGRREGWG AGWRSGLRVG GGG 103

- (2) INFORMATION ON SEQ ID NO. 248:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

GSRRRDGGGA GAAPVAPRAL GRRARAGRCS EDEGGGGAQR VWGEQPVLAS GQSPPGQEGS60 FTRVWTRASL PTLGQVLQPG GVHVQV

- (2) INFORMATION ON SEQ ID NO. 249:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 154 amino acids

    - (B) TYPE: Protein (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

ARGGAMAAGL ARLLLLIGLS AGGPAPAGAA KMKVVEEPNA FGVNNPFLPQ ASRLQAKRDP 60 SPVSGPVHLF RLSGKCFSLV ESTYKYEFCP FHNVTQHEQT FRWNAYSGIL GIWHEWEIAN120 NTFTGMWMRD GDDCRSRSRQ SKVELACASP SNCV

- (2) INFORMATION ON SEQ ID NO. 250:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

PLDAVARART RQLHLALPAP GTAVVTVPHP HAREGVVGDL PLVPDAEDPT VGVPAEGLLV60 LGHVVERAEL ILVRGLHQAE ALARESEEMH GSRHG 95

- (2) INFORMATION ON SEQ ID NO. 251:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 240 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

KVTDGHTRTP RSGVPRQHEA GSPGLTASHA MSIHLAGSLT AMDSICASER SQGVWRAPTP 60 GCQGLSPGPR PGELPGGSSP EERLGRLAVA GPPRGAQNVS QAGPEAEAPP LRFGHAWGAQ120 TPRLGAPGPW TPLPTLPSHI PPFWSQTPAQ RKEGFTEEGQ GRAWPQGGDE DISGPGSCRL180 LWEEEPCVCK LLGLAARPTA GPSLDPCTWP SSCPLAAPGL GTGIEPRGLG WLGQGRDREG240

- (2) INFORMATION ON SEQ ID NO. 252:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 216 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GLVMPGELRR PGLGPQAHGL PSPLCPPIFP LFGPRHQHKE RRGSQRKARA EPGPREGMRT 60 FPVQVAAGCS GRKSHASVNC WGWRPAPLQG PALTPARGHP AALWLPLALA QASSLEGWAG120 WARAGTGRGS TSDPDVGWLC PPRREAQQTS YTKAKSTIGE PRSHFMGRRP RPQGPQSKAR180 GRFIPEDSPP GAAPAWGGVS RPLGCLSVCG TPWSTP 216

- (2) INFORMATION ON SEQ ID NO. 253:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 218 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

VLRRLYIYIL YITNMKWFST QPLWLNTKQR SHRRGPGPPP APLSGVLGSR GLPHHPSQGW 60 GRAGPRAGAN VAWNSNCIVR WVGGQWARGC SQPGPFTTNL AMTCGGPWGS GCLLGSTLSE120 VSPWAPPSCP QGHPVLPTRL WAWGLQDPLC RVRVGAGHGS RHQPDAPVGV ARSWDGVVRN180 TAPKTQNKNT TNGRRSPPPT EVGFEPLLIF PVSFLQPW 218

- (2) INFORMATION ON SEQ ID NO. 254:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 79 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

RDGGGAGAAP VAPRALGRRA RAGRCSEDEG GGGAQRVWVS SLAGWRLERG TARARSPLTL60 PLPVGGTTRS CLRPVASRP 79

- (2) INFORMATION ON SEQ ID NO. 255:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 79 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi)	SEQUENCE	DESCRIPTION	ON: SEQ	ID NO:	255:	
LGLEATGLRQ	ERVVPPTGSG	KVSGERARAV	PRSSRQPAP	RL LTQTE	RWAPPP	PSSSLHLPAR60
ARRPRARGAT	GAAPAPPPS			٠.		79

- (2) INFORMATION ON SEQ ID NO. 256:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 79 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

WPGGDWPEAR TGCSTYGKRQ GQRGTGPGRP PLEPPAREAA HPNALGSSTT FIFAAPAGAG60 PPAESPRSNR SRASPAAIA

- (2) INFORMATION ON SEQ ID NO. 257:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 51 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GHLGGPTGSV CSRILLASSP FYMNCCINKH RVPETTEVII LPTECWPGQA W

- (2) INFORMATION ON SEQ ID NO. 258:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 49 amino acids
    - (B) TYPE: Protein

(C) STRAND: individual

(vi)

ORIGIN

(A) ORGANISM: HUMAN

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:
GGGFLGQIDK SKDNISLVTV IQLHSYTVAL FGLSHEEVLV TNYVFVGCF 49
(2) INFORMATION ON SEQ ID NO. 259:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 48 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(Vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:
AFTRNTTNKV SDMLANQARL RSLRRPNWLC LLKDSSGLVS ILHELLHK 48
(2) INFORMATION ON SEQ ID NO. 260:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 179 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes

PGISVSVDKM ESSPFNRRQW TSLSLRVTAK ELSLVNKNKS SAIVEIFSKY QKAAEETNME 60 KKRSNTENLS QHFRKGTLTV LKKKWENPGL GAESHTDSLR NSSTEIRHRA DHPPAEVTSH120 AASGAKADQE EQIHPRSRLR SPPEALVQGR YPHIKDGEDL KDHSTESKKM ENCLGESRH 179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

(2) INFORMATION	ОИ	SEQ	ID	NO.	261:
-----------------	----	-----	----	-----	------

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

  QATLLLEPKL TKKNKSTPDL DSGHLLKPSF RVDIPTSRTV RILKTTQQKV KKWKIV
- •
- (2) INFORMATION ON SEQ ID NO. 262:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

DSAPSPGFSH FFFNTVRVPF LKCWERFSVL LLFFSMFVSS AAFWYLENIS TIADDLFLLT60 RESSLAVTLN DSEVHCRLLN GDDSILSTDT EIPG 94

- (2) INFORMATION ON SEQ ID NO. 263:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

VMSDPADKAA RADSARAARG KRKKNVEENM AYSALMEVAG YCLIERMLWN PMLKIKSVWL60 CSYAVMVIPR QLAKV

- (2) INFORMATION ON SEQ ID NO. 264:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 74 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

AMFSSTFFFL LPRAARAESA RAALSAGSLI TYAFYKRLPK KKLLTRNVDK PLKANKQQTV60 VFAFSYSWQA EVRA

- (2) INFORMATION ON SEQ ID NO. 265:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 63 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

DSKAFSLLSS NQPLPSKLSR PCFPPHFFFF YLEPLEPNRL EPPCLLDHSS PTHFIKGYPK60 RNC

- (2) INFORMATION ON SEQ ID NO. 266:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

RRGSGSRSSM APVLASMLWM STRGTAMTST SLCTSRARSR PMPSSSSPTP TAWRCCCATR60 TRVSTSTRTG ASLRMWCCSG GRCLLLWPTS APTR 94

- (2) INFORMATION ON SEQ ID NO. 267:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 254 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

GDRKPLYHYG RGMNPADKPA WAREVKERTR MNKQQNSPLA KSKPGSTGPE PPSPQASPGP 60
PGLPWAPKPY HKFMAFKSFA DLPHRPLLVD LTVEEGQRLK VIYGSSAGFH AVDVDSGNSY120
DIYIPVHIQS QITPHAIIFL PNTDGMEMLL CYEDEGVYVN TYGRIIKDVV LQWGEMPTSV180
AYICSNQIMG WGEKAIEIRS VETGHLDGVF MHKRAQRLKF LCERNDKVFF ASVRSGGSSQ240
VYFMTLNRNC IMNW 254

- (2) INFORMATION ON SEQ ID NO. 268:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 231 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GKKHLVIPLT QELEPLSSFV HEDPVEVARL HRADLNGFLT PAHYLVGADV GHRSRHLPPL 60 QHHILNDAPV RVDVDTLVLV AQQHLHAVGV GEEDDGMGRD LALDVHRDVD VIAVPRVDIH120 SMEASTGAID DLEPLPLLYC QVDQQRAVGE VGKGLEGHEF VVGFGGPGEA WGPWGGLGAG180 GLRPRAAWLA LGQGRVLLLV HPCSLFYLSG PGWFVSGIHA PTIMVQGLPV P 231

- (2) INFORMATION ON SEQ ID NO. 269:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 454 amino acids
      - (B) TYPE: Protein
      - (C) STRAND: individual
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GAGCTSPGLW ARKAAARCLP TYPSRAQPSN VGRRRRRPG LGALAAGVPA MAESVERLQQ 60
RVQELERELA QERSLQVPRS GDGGGGRVRI EKMSSEVVDS NPYSRLMALK RMGIVSDYEK120
IRTFAVAIVG VGGVGSVTAE MLTRCGIGKL LLFDYDKVEL ANMNRLFFQP HQAGLSKVQA180
AEHTLRNINP DVLFEVHNYN ITTVENFQHF MDRISNGGLE EGKPVDLVLS CVDNFEARMT240
INTACNELGQ TWMESGVSEN AVSGHIQLII PGESACFACA PPLVVAANID EKTLKREGVC300
AASLPTTMGV VAGILVQNVL KFLLNFGTVS FYLGYNAMQD FFPTMSMKPN PQCDDRNCRK360
QQEEYKKKVA ALPKQEVIQE EEEIIHEDNE WGIELVSEVS EEELKNFSGP VPDLPEGITV420
AYTIPKKQED SVTELTVEDS GESLEDLMAK MKNM

- (2) INFORMATION ON SEQ ID NO. 270:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

KLTVPKFNRN FNTFCTKIPA TTPIVVGRLA AQTPSRFRVF SSIFAATTSG GAHAKQADSP 60 GIISCICPET AFSLTPDSIH VCPSSLQAVF IVIRASKLST QLRTRSTGFP SSNPPLLILS120 MKC

- (2) INFORMATION ON SEQ ID NO. 271:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 176 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

CSSEYVLLE LYLILLDEVG RKVYSYWLVP PCHNQRVATY QCHILSAFQQ SHYLLHQHLL 60 LLRQRYGFSH SRLQFPFVSM PSSGCRDSNP PPLSSSSRCG PGRPLRRRSS GPADSSPGQV120 PAPAPGPAAA GAPQTPPWLG LRPPTLPARA FAAAFAPRCS AGPARGTWGG TSPLPS 176

- (2) INFORMATION ON SEQ ID NO. 272:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

- (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

EARQAWTGAK GAGSLTFSSL QSGHLASGSQ SPESTKAPGT PPTPSYPGTP SRQLLWQWVQ 60 PRPALPASSP CSRHQLYLPR QAMSWLLSPA PSVPLDFSGA SPVWATLCFP HPRLPHR 117

- (2) INFORMATION ON SEQ ID NO. 273:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

APALPPPAGN VLASQPSTIC SPRLLRGQPS LGHPLFPSSS APTQVTDPAD SFSLGKVGCC60 LTSPSSPPPI HTHRHPPTPG RLVSHM 86

- (2) INFORMATION ON SEQ ID NO. 274:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 177 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

EARTLPAGGG RAGAYCRERR LAVLAWAGPT AITVAYLGSL GRMEWVGCQG LWCFLVIGTL 60 MPSAHFAKKK KLMTLLPWLL SMLAWPPRVG GTSPLLAEAG EQVLSYDPIH QAGVLSPSGH120 HSSQHQGPVG LGQGSEKGWQ EVPRSSQPGR GTNALNTSKL RDPKVSTPGS GLPPHRH 177

(2	) INFORMATION	ON	SEQ	ID	NO.	275:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

QFPGPSVPEQ STSVSVTTSC LFPSLHLLQF IYMLLLLVHF CLPYQAVNEG RNLVCFIHHH60 VPSAWHIVGL H

- (2) INFORMATION ON SEQ ID NO. 276:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 102 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

FFFFFFFFF FFFCLINMSI YLAPDGNTKS WQWEWKGSLS QILPYYVDPK AGLGSKAHKP 60 PKQIFIEHLD YYRPSILLGT MGDVKEVISH MICLQGAKNA SG 102

- (2) INFORMATION ON SEQ ID NO. 277:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 65 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

GVIESRRVLS RGVIRFIFKQ PNPGRCGPIL SALKKIPFPY LPASIMSVEE SNCGSFEGDG60 PFFPV 65

- (2) INFORMATION ON SEQ ID NO. 278:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 65 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

FFFFFFFFF FFLFNKYEHL FGTRWQYKIL AVGVERFSLS NTSILCRPKG RTWQQGSQTT60 QTNIY

- (2) INFORMATION ON SEQ ID NO. 279:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 489 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

LADSFPGSSP YEGYNYGSFE NVSGSTDGLV DSAGTGDLSD GYQGRSFEPV GTRPRVDSMS 60
SVEEDDYDTL TDIDSDKNVI RTKQYLYVAD LARKDKRVLR KKYQIYFWNI ATIAVFYALP120
VVQLVITYQT VVNVTGNQDI CYYNFLCAHP LGNLSAFNNI LSNLGYILLG LLFLLIILQR180
EINHNRALLR NDLCALECGI PKHFGLFYAM GTALMMEGLL SACDHVCPNY TNFQFDTSFM240
YMIAGLCMLK LYQKRHPDIN ASAYSAYACL AIVIFFSVLG VVFGKGNTAF WIVFSIIHII300
ATLLLSTQLY YMGRWKLDSG IFRRILHVLY TDCIRQCSGP LYVDRMVLLV MGNVINWSLA360
AYGLIMRPND FASYLLAIGI CNLLLYFAFY IIMKLRSGER IKLIPLCIV CTSVVWGFAL420
FFFFQGLSTW QKTPAESREH NRDCILLDFF DDHDIWHFLS SIAMFGSFLV LLTLDDDLDT480
VQRDKIYVF

- (2) INFORMATION ON SEQ ID NO. 280:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 182 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

APLCHRPVTL SCCGDESQHR CPALDGSRTA RSSLGLAWDS HGVAWNLAAA LCRGAGLLPW 60 DPQMLAKLLL SSQCWGLPWA PVLWLSICPF ARGRMEGTPS PFHALHFARP PPHNAPAWDL120 RPLFPPILPL QGLVWGLNLC PVSGPQFSLG CPWLPSLPIP VSQDGWGYEI LGVGQLVPDF180 WC

- (2) INFORMATION ON SEQ ID NO. 281:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 536 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

ARPGCPAAIQ CWAAVLGLIP TARQSDRSMT QRSSGPLEVK RRAQLLLEDI DLVPLHSIQV 60 VIQCQQHQEG PEHGDGGEV PDVVVVKEVE EDAVPVVLPR LCRGFLPGAE SLEEEEEREA120 PDHGGANDAE QGDELDPLPT PELHDDVEGE VKEQVADANG QQVGSEIIGA HDKPIGSQRP180 VDDVAHDQQH HAVHVERPAA LPDAVCVEHV EDAAEDPRVQ FPPAHVIELR AEEQGGDDVN240 DGEDDPERRV PFAKDHAQHR EEDDNGQAGV GTVGAGVDVR VPLLVELQHA ESGDHVHERC300 VKLEIGIVGA HMIASTEQPL HHQGCAHGVE KPKVFGDPTF QGTEVIAQQG PVVVDLPLQD360 DEQEKQPQQD VPQVAEDVVE GAEIAQWVGA EEVVVADVLI PCDIHHRLVG DHQLHHRKGI420 EDSNGGNVPE VDLVLFPQNT LVLPCQVSHI EVLLGANDIL VGIDVGQCVV VILLHRAHGV480 HSGPSTYRFK GAALVTVREV PSASAVNQTI GRSRNILKGA IVVTLIRGTA RKRISQ 536

- (2) INFORMATION ON SEQ ID NO. 282:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 551 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

PLSSPSCCRY RRCCRRLRPP LRSVVQPGPR TMSLSRSEEM HRLTENVYKT IMEQFNPSLR 60
NFIAMGKNYE KALAGVTYAA KGYFDALVKM GELASESQGS KELGDVLFQM AEVHRQIQNQ120
LEEMLKSFHN ELLTQLEQKV ELDSRYLSAA LKKYQTEQRS KGDALDKCQA ELKKLRKKSQ180
GSKNPQKYSD KELQYIDAIS NKQGELENYV SDGYKTALTE ERRRFCFLVE KQCAVAKNSA240
AYHSKGKELL AQKLPLWQQA CADPSKIPER AVQLMQQVAS NGATLPSALS ASKSNLVISD300
PIPGAKPLPV PPELAPFVGR MSAQESTPIM NGVTGPDGED YSPWADRKAA QPKSLSPPQS360
QSKLSDSYSN TLPVRKSVTP KNSYATTENK TLPRSSSMAA GLERNGRMRV KAIFSHAAGD420
NSTLLSFKEG DLITLLVPEA RDGWHYGESE KTKMRGWFPF SYTRVLDSDG SDRLHMSLQQ480
GKSSSTGNLL DKDDLAIPPP DYGAASRAFP AQTASGFKQR PYSVAVPAFS QGLDDYGARS540
MSSADVEVAR

- (2) INFORMATION ON SEQ ID NO. 283:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 185 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

AGEAAGQPGS PPSHQLAKCP PLTQGYPRLH GHVTRGVYPQ EAAPQPWAAQ PLGLALQGPA 60 PHSARPCLEQ LGSSPGQTQV GQDQAAGAWM FSTQERTDDD RTGYMGRAGE ATRWAALQMW120 PSAEEGGRPV VGHCRLQLDV GKGILTLVRR LRIWPLPHRR CSWTALHSHP GPGRRARPH180 CRASA

- (2) INFORMATION ON SEQ ID NO. 284:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 518 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

SGGSESGHFH IGAAHGPRSI VIQALGEGGH GHTVGPLLEA AGRLGGEGPG GGAVIGGWDG 60
QVVLVQEVAR AAALPLQAH VQPVTAIAVQ DPGVGEGKPA PHLGLLTLSV VPAIAGLRHQ120
QGNEVTLLEA QEGAVVPSSV GEDGLHPHTA IALQAGCHGA RARQSLVLGG GIAVFWGHAL180
AHGECVGVGV AELALRLRRR QGFGLGSLAV SPRAVVLAIR ACDAVHDGCA LLGRHPPHER240
CQLGGHRQGL GPRNGVGNDQ VGLGGRQGAG EGGAVAGHLL HELHRALRDL AGVGTGLLPQ300
RQLLRQQLLA LGVVGRGVLG HGALLLHQEA EAPALLCQCG LVAVGHVILQ LALLVADGVD360
VLQLLVRVLL RILAALALLP KLLQLSLTLV QGVAFAPLLS LVFLQRSTQI PGVQLHLLLQ420
LRKQLVVKRL QHFFQLILDL PVDFSHLEEN VSEFFGALAL AGQLPHLHQG VKVAFGCIRH480
TCQCLLVILP HGDEVPEARV ELLHDGLIDI FREPVHLL

- (2) INFORMATION ON SEQ ID NO. 285:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 217 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

VREAARREQR YQEQGGEASP QRTWEQQQEV VSRNRNEQES AVHPREIFKQ KERAMSTTSI 60 SSPQPGKLRS PFLQKQLTQP ETHFGREPAA AISRPRADLP AEEPAPSTPP CLVQAEEEAV120 YEEPPEQETF YEQPPLVQQQ GAGSEHIDHH IQGQGLSGQG LCARALYDYQ AADDTEISFD180 PENLITGIEV IDEGWWRGYG PDGHFGMFPA NYVELIE

- (2) INFORMATION ON SEQ ID NO. 286:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 162 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

AGASGRLWLP SAFICLFSFS LASKGWWPPL FRMTLGNSER RELFLAEFVT KVRVDHGGLA 60 AGNLSCWSLL CAPHSISLSL CLGYGKWGCR WPSSHPGYSK TADTTCSSTR LTRCLQAPVC120 ASTDSDFRKS NTEWPWPVVF PYFLSQLIRV SEEQICFWTK KK 162

- (2) INFORMATION ON SEQ ID NO. 287:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 173 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

LLACRGWPGR RWWEELNSGK VMYAFCRVKD PNSGLPKFVL INWTGEGVND VRKGACASHV 60 STMASFLKGA HVTINARAEE DVEPECIMEK VAKASGANYS FHKESGRFQD VGPQAPVGSV120 YQKTNAVSEI KRVGKDSFWA KAEKEEENRR LEEKRRAEEA QRQWSRSAGS VSA 173

- (2) INFORMATION ON SEQ ID NO. 288:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 597 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

EKCGQYIQKG YSKLKIYNCE LENVAEFEGL TDFSDTFKLY RGKSDENEDP SVVGEFKGSF 60 RIYPLPDDPS VPAPPRQFRE LPDSVPQECT VRIYIVRGLE LQPQDNNGLC DPYIKITLGK120 KVIEDRDHYI PNTLNPVFGR MYELSCYLPQ EKDLKISVYD YDTFTRDEKV GETIIDLENR180 FLSRFGSHCG IPEEYCVSGV NTWRDQLRPT QLLQNVARFK GFPQPILSED GSRIRYGGRD240 YSLDEFEANK ILHQHLGAPE ERLALHILRT QGLVPEHVET RTLHSTFQPN ISQGKLQMWV300 DVFPKSLGPP GPPFNITPRK AKKYYLRVII WNTKDVILDE KSITGEEMSD IYVKGWIPGN360 EENKQKTDVH YRSLDGEGNF NWRFVFPFDY LPAEQLCIVA KKEHFWSIDQ TEFRIPPRLI420 IQIWDNDKFS LDDYLGFLEL DLRHTIIPAK SPEKCRLDMI PDLKAMNPLK AKTASLFEQK480 SMKGWWPCYA EKDGARVMAG KVEMTLEILN EKEADERPAG KGRDEPNMNP KLDLPNRPET540 SFLWFTNPCK TMKFIVWRRF KWVIIGLLFL LILLLFVAVL LYSLPNYLSM KIVKPNV 597

- (2) INFORMATION ON SEQ ID NO. 289:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 120 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

DQHSCFKMSP DSKASHNPSF PKMGVESDME DETTAWMNLK PTKSCTSTSG PLKSGLLFTS 60 SGLRGWSLST WKQGLCTAPS SPTFPRENFR CGWMFSPRVW GHQALLSTSH PGKPRNTTCV120

- (2) INFORMATION ON SEQ ID NO. 290:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 289 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

ETQVVIQRKL VIVPYLNDQP GWDSKFRLVN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60 FTIQRSVMDI CFLFVFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVPDDH TQVVFLGFPG120 CDVERRAWWP QTLGENIHPH LKFSLGNVGL EGAVQSPCFH VLRDQPLSPE DVKSKPLFRG180 PEVLVQDFVG FKFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISPGIDSR240 NTVLLWYAAV GPKAGKESVF QINNCFSYFF IPGKGVIIID RNFQVFFLR 289

- (2) INFORMATION ON SEQ ID NO. 291:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 201 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

GTGDGSKEIN IVWGIQVPIF HNGPWVSTNH PVARFPRITS LASEGIIVPS TSTIRGMGVW 60 RASCGDCRAD STSSIAQDRG PGLTIGHQAL GSLVWVGESW GQTWGEYLGG PRWLGWLDLR120 QSWALSISEE VVKKRDFLFH FLNFLCMLVE DMFAHKLRTL EFLATERTQP LILAQFLRVG180 GDELLHFLLW VFAPHLLGLF L 201

- (2) INFORMATION ON SEQ ID NO. 292:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 171 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

SVIFFKIGFC EGRLVGRGGV PGSEAQSCVL SSSVWISLAA SLMSLRTICL CWVMPLMLRT 60 RRVRSLFTPG LSSHSRRRMF CRFQQISLML TLRSKVTQPR RKNLLSGWGS ESATRIKPGY120 LLQREMISAR EMLGAMLRMK REQVLCSGRG LHSSPAASLG FSHSSSLGFS F 171

- (2) INFORMATION ON SEQ ID NO. 293:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 485 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

EKEKPKEEEW EKPKDAAGLE CKPRPLHKTC SLFMRNIAPN ISRAEIISLC KRYPGFMRVA 60
LSEPQPERRF FRRGWVTFDR SVNIKEICWN LQNIRLRECE LSPGVNRDLT RRVRNINGIT120
QHKQIVRNDI KLAAKLIHTL DDRTQLWASE PGTPPLPTSL PSQNPILKNI TDYLIEEVSA180
EEEELLGSSG GAPPEEPPKE GNPAEINVER DEKLIKVLDK LLLYLRIVHS LDYYNTCEYP240
NEDEMPNRCG IIHVRGPMPP NRISHGEVLE WQKTFEEKLT PLLSVRESLS EEEAQKMGRK300
DPEQEVEKFV TSNTQELGKD KWLCPLSGKK FKGPEFVRKH IFNKHAEKIE EVKKEVAFFN360
NFLTDAKRPA LPEIKPAQPP GPAQILPPGL TPGLPYPHQT PQGLMPYGQP RPPILGYGAG420
AVRPAVPTGG PPYPHAPYGA GRGNYDAFRG QGGYPGKPRN RMVRGDPRAI VEYRDLDAPD480
DVDFF

- (2) INFORMATION ON SEQ ID NO. 294:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 368 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

ESSGFQAIGR AEDDARSCWV KTSESTRPYQ LLRRRRPTLI TYRIFRHRH KDTSSGDHLT 60 CRLDPQAKDL KDGTQEEATK RQEAPVDPRP EGDPQRTVIS WRGAVIEPEQ GTELPSRRAE120 VPTKPPLPPA RTQGTPVHLN YRQKGVIDVF LHAWKGYRKF AWGHDELKPV SRSFSEWFGL180 GLTLIDALDT MWILGLRKEF EEARKWVSKK LHFEKDVDVN LFESTIRILG GLLSAYHLSG240 DSLFLRKAED FGNRLMPAFR TPSKIPYSDV NIGTGVAHPP RWTSDSTVAE VTSIQLEFRE300 LSRLTGDKKF QEAVEKVTQH IHGLSGKKDG LVPMFINTHS GPVSPTWGVF HGGAPGADSL360 LLSYLFER

- (2) INFORMATION ON SEQ ID NO. 295:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

ALRSPPRMRI VLSNRLTSTS FSKCNFFDTH FLASSNSFLR PKIHMVSSAS ISVRPRPNHS60 LKDLDTGFSS SWPHANLRYP FHACRKTSIT PFWR 94

- (2) INFORMATION ON SEQ ID NO. 296:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

LLRHPLPGFL KFFPQTQDPH GVQRVDQCET EAKPLTEGPG HRLQLVMAPC KLAVSFPCMQ60 EDVNHALLAI VQMHWCALCP GRWQGRLGGH FCSS 94

- (2) INFORMATION ON SEQ ID NO. 297:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 146 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

SGPLLAGPAT LTGRMSEVRL PPLRALDDFV LGSARLAAPD PCDPQRWCHR VINNLLYYQT 60

NYLLCFGIGL ALAGYVRPLH TLLSALVVAV ALGVLVWAAE TRALCAAAAA ATLQPAWPQC120 LPSASWCSGS RAALAPSCSA SPGRCF 146

- (2) INFORMATION ON SEQ ID NO. 298:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 152 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TQRHSHPPFS MLIPKLGPGA RHSQILNPGP KLFQTPPYLP TQVKTLPNLE LRTQVFHAPV 60 WMESGILTVG PLVQVIPTLT SPICLPPALL RHFAPHPNVP HHRQPRGEVG TGLSREWGVY120 VSVAATIKPV ASLMPKKKKK STGRKYSSSS RP 152

- (2) INFORMATION ON SEQ ID NO. 299:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 172 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

RTTTTTIFAA GRLFFFFWHE RCNRLYCCSN TNIYAPFPAE ACPHLTPWLS MVWNIGVRGK 60 MPKQSWREAN GTGEGRDHLD QGSNSQDTRL HPHRGMEHLG SEFKIWQCLD LGWKVGWGLE120 KLWSRVQDLR VPCSRPQFGD EHGEGWMGVS LGSQFEIGHG CSGLKPQFWG WM 172

- (2) INFORMATION ON SEQ ID NO. 300:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 178 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

WFWRESYWQT IKVDLQVEHP YQFLLKYAKQ LKGDKNKIQK LVQMAWTFVN DSLCTTLSLQ 60 WEPEIIAVAV MYLAGRLCKF EIQEWTSKPM YRRWWEQFVQ DVPVDVLEDI CHQILDLYSQ120 GKQQMPHTP HQLQQPPSPE PPTPLPGPCG CWASHLKEGK VVQPEPVEQC PVWPPKPK 178

- (2) INFORMATION ON SEQ ID NO. 301:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 113 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

CISQDVCANL KYKNGPPNPC IGDGGSSLFK MSRSTFWKTS ATKSWIFTHK ENNRCLITPP 60 ISCNSPHLLS LPPRCLGPVV AGPPTSRRGR LYSPNPWSNA LSGLQNQNKT GSL 113

- (2) INFORMATION ON SEQ ID NO. 302:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 90 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

GGRPSNHRAQ AAGWEAQEMG AVAADGGCDE ASVVFLVSKD PGFGGRCLPK RRPGHLEQTA60 PTISYTWVWR SILVFQICTN VLRDTSLLLL 90

- (2) INFORMATION ON SEQ ID NO. 303:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 158 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

TQVMVQSMFA PTDTSDMEAV WKEAKPEDLM DSKLRCVFEL PAENDKPHDV EINKIISTTA 60 SKTETPIVSK SLSSSLDDTE VKKVMEECKR LQGEVQRLRE ENKQFKEEDG LRMRKTVQSN120 SPISALAPTG KEEGLSTRLL ALVVLFFIVG VIIGKIAL

- (2) INFORMATION ON SEQ ID NO. 304:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 112 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

VNKALPFISK ALGQSVNTRL SLMTSTSDAA TVQFLWASDS VHQSQGADGL DRTEDTESSL 60 GREWATWGLL CGADRTPQHA GLQLPKGQHQ QARKGVILRE VIQHHVPRPT NV 112

- (2) INFORMATION ON SEQ ID NO. 305:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 105 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

FKGKTCEMSS YINFFLHMVM INLNPMIWWI HQSNLPSCAC YLYKAIFPII TPTIKNKTTR 60 AKSRVLRPSS FPVGANAEMG LLLCTVFLIR SPSSSLNCLF SSRSL

- (2) INFORMATION ON SEQ ID NO. 306:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 126 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

RPPQRTLRHS AQLGAAPAAL PQPLWELPRA HGSQRQPGPG EAADHAEQER EEAAERPGSS 60 PEEGQEGSGA FGGHTGHRAC ARCLGRGALG GRIPCGLLCQ LFRRDGCPAD SEVQHHIHQH120 WQQLLP 126

- (2) INFORMATION ON SEQ ID NO. 307:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 240 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
      - (D) TOPOLOGY: linear
  - MOLECULE TYPE: ORF (ii)
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

NVGRCCEAQA RAGAASLNAS LDGLHNALFA TQRSLEQHQR LFHSLFGNFQ GLMEANVSLD 60 LGKLQTMLSR KGKKQQKDLE APRKRDKKEA EPLVDIRVTG PVPGALGAAL WEAGSPVAFY120 ASFSEGTAAL QTVKFNTTYI NIGSSYFPEH GYFRAPERGV YLFAVSVEFG PGPGTGQLVF180 GGHHRTPVCT TGQGSGSTAT VFAMAELQKG ERVWFELTQG SITKRSLSGT AFGGFLMFKT240

- (2) INFORMATION ON SEQ ID NO. 308:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

KAGIEGHRGS CLPERRAQGT WHRPCDPYVH QRLRFLLVPL PGSFQVFLLL LPFPAQHGLQ 60 LPQVQADVGF HEPLEVPKEA VEEPLVLLQA ALSGEECVVE AVKGGVEGGG PGPGLGLAAP120 PDI

- (2) INFORMATION ON SEQ ID NO. 309:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 84 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

PTTTLVIPLF FLSSRKRKQK DSFQTALCSL HCSFPKQAAS TGKAHVVTPY FSEVLLFHGV60 TLLSESKFRK QVLPLADKNH TSFL 84

- (2) INFORMATION ON SEQ ID NO. 310:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 128 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

CDRVPLFLSY WCAVADSWLT ASSVSHVKGI LSPQPTECAP PGPANCFFNF FFFFFLVET 60 GSPSVAQDGL ELLGSSNPPT LASQSAEITG MSHYAQPEQD DLNLINSTPK QQLSLSQGCQ120 GGLCEGKD

- (2) INFORMATION ON SEQ ID NO. 311:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

WVAGRRHLLS VQTKSLQVLG LDLCVTPESQ CIRYLYKKLV WFLSAKGKTC FLNLLSDNKV60 TPWKRRTSEK YGVTTWAFPV LAACFGKLQC RLQRAV 96

- (2) INFORMATION ON SEQ ID NO. 312:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 57 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:	
ISTSIAALWL PGGQDAGGGA LWPLCGSRGL CVSDRFPGNF RARLTSWKFK YSIALEF	57
(2) INFORMATION ON SEQ ID NO. 313:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 52 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:	
SAHQLQHCGY QGVRMRAVEP SGLCVVAEDS VSATVFRETS GRDSHLGNSN TQ	52
(2) INFORMATION ON SEQ ID NO. 314:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 43 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:	

NSRAIEYLNF QDVSLARKFP GKRSLTQSPR LPHKGQRAPP PAS

- (2) INFORMATION ON SEQ ID NO. 315:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 247 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSGLK HEDKRGGSGS 60 HNWGTVKDEL TESPKYIQKQ ISYNYSDLDQ SNVTEETPEG EEHHPVADTE NKENEVEEVK120 EEGPKEMTLD EWKAIQNKDR AKVEFNIRKP NEGADGQWKK GFVLHKSKSE EAHAEDSVMD180 HHFRKPANDI TSQLEINFGD LGRPGRGGRG GRGGRGGRG PNRGSRTDKS SASAPDVDDP240 EAFPALA

- (2) INFORMATION ON SEQ ID NO. 316:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

FMKNKSLLPL PISTFIWFSD IKFYFCPVLI LNSLPLIQSH LFWTLLFYLF NFILLIFSVC60 HWMMFFTFRC FLSHI 75

- (2) INFORMATION ON SEQ ID NO. 317:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 78 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

SFGILKHAKA LNRRVHKGTR VVLWHPVKPE LGMPLGHPHQ EQKHLTCRSC CHGLGAHHAH60 VHLVLPCRHV LGGQGLQN 78

- (2) INFORMATION ON SEQ ID NO. 318:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 235 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

LHLGAQRALA PGLFRLQGML RALLGRQLFR ARGPPVVREP LPRTTRLAVR HVWPPCDRPL 60 RVGPGSPLPP GPLHMHLLPA PAHQGVLPGA RRQALLPALL PEALRLTARS ARPLPRRPRP120 PGKAGSSRPR GLALRAGGPT HWRAPPLRYY ESSGVKFRNG PARPKPTRPQ SGLHTDKNSR180 AGLHSIPTLE GAPLLGEGPC NSSESEARPG RPCSLHPHCS VHFFYLHKHT HSTSK 235

- (2) INFORMATION ON SEQ ID NO. 319:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 478 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

GSRPPPCSPR ATGPRPAMED LDALLSDLET TTSHMPRSGA PKERPAEPLT PPPSYGHQPQ 60
TGSGESSGAS GDKDHLYSTV CKPRSPKPAA PAAPPFSSSS GVLGTGLCEL DRLLQELNAT120
QFNITDEIMS QFPSSKVASG EQKEDQSEDK KRPSLPSSPS PGLPKASATS ATLELDRLMA180
SLSDFRVQNH LPASGPTQPP VVSSTNEGSP SPPEPTGKGS LDTMLGLLQS DLSRRGVPTQ240
AKGLCGSCNK PIAGQVVTAL GRAWHPEHFV CGGCSTALGG SSFFEKDGAP FCPECYFERF300
SPRCGFCNQP IRHKMVTALG THWHPEHFCC VSCGEPFGDE GFHERGRPY CRRDFLQLFA360
PRCQGCQGPI LDNYISALSA LWHPDCFVCR ECFAPFSGGS FFEHEGRPLC ENHFHARRGS420
LCATCGLPVT GRCVSALGRR FHPDHFTCTF CLRPLTKGSF QERAGKPYCQ PCFLKLFG 478

- (2) INFORMATION ON SEQ ID NO. 320:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 285 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

EQGLGVWRTR LFREGAASGG EGEPSGLSAE ELQEAGLAVG LAGALLEGPL GERAQAEGAC 60
EVVRVEAATQ GRHAAAGHRE ATRGAQRAAS CVEVVLAQRA ALVLEKAASR EGREAFPADE120
TVRVPERAER RDVVIQDGAL AALAARGEQL QEVPAAVGAA LALVETLISE GLPATDAAEM180
LWVPVSAQGG HHLVSDGLVA EATSWREALK VALGAEGGSI LLEEAAASQG GGTASANEVL240
GVPGAAQSRH HLPSNRFIAG ATEAFGLGGN TPAAEVGLQQ PQHGV 285

- (2) INFORMATION ON SEQ ID NO. 321:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GLHLQPLLWR QSTEEEVREE GQALTEPKSC GAQGGAQHRG LTPCPTGNGL GLAQPKIPAL60 SNSWRVDSVL ACLVSSDIFH TVEQNHQPCT DVTLCRKRP

- (2) INFORMATION ON SEQ ID NO. 322:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

ETQSSQRLTC PRSLGLDLSL RLRLQNPHSI CYISQGWGQG SCEQKEKYQL LKGLGFVGRA60 RQGQRGIQNK GASTSAWDGP IHSGRGCGVS PVLRNHLAS 99

- (2) INFORMATION ON SEQ ID NO. 323:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 83 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

SNPKAPVSMW VKGPTMGTYT QEDESSLASE SDCLPQTPPQ NRLLSHLPLH SDKTQAHIPG60 PGVFACICID GNAGPAKAFF YIK 83

- (2) INFORMATION ON SEQ ID NO. 324:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 111 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

VFPTVLRGVL VPSSVTSKPG LIVPIGDEGG MRRSHLQLLS VERTSGTEKN RGPHGSLEGR 60 GTRVGELIAE RRDVQRPSAP LSWDVNRIFP STPSLPPVLP LFFFPSIKRC I 111

- (2) INFORMATION ON SEQ ID NO. 325:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 272 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

SSRASGITRA ARPCPAKNEG PSKAFVNCDE NSRLVSLTLN LVTRADEGWY WCGVKQGHFY 60 GETAAVYVAV EERKAAGSRD VSLAKADAAP DEKVLDSGFR EIENKAIQDP RLFAEEKAVA120 DTRDQADGSR ASVDSGSSEE QGGSSRALVS TLVPLGLVLA VGAVAVGVAR ARHRKNVDRV180 SIRSYRTDIS MSDFENSREF GANDNMGASS ITQETSLGGK EEFVATTEST TETKEPKKAK240 RSSKEEAEMA YKDFLLQSST VAAEAQDGPQ EA

- (2) INFORMATION ON SEQ ID NO. 326:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 241 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TLVFGRLRTK PFRIPGFLQR KRRWQIQEIK PMGAEHLWIP AALRNKVEAP ERWSPPWCPW 60
AWCWQWEPWL WGWPEPGTGR TSTEFQSEAT GQTLACQTSR TPGNLEPMTT WEPLRSLRRH120
PSEEKKSLLP PLRAPQRPKN PRRQKGHPRR KPRWPTKTSC SSPAPWPPRP RTAPRKPRRC180
RRLLPAPMTI TFRIMSILGP SAPGDPTPCS NTCLGFSYCP QRRAGPLLSD IKAWPNCSYW240
G

- (2) INFORMATION ON SEQ ID NO. 327:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 121 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

AVVRVTWYKG EGITLPPVLT PALVRGESIP IRLFLAGYEL TPTMRDINKK FSVRYYLNLV 60 LIDEEERRYF KQQEVVLWRK GDIVRKSMSH QAAIASQRFE GTTSLGEVRT PSQLSDNNCR120

- (2) INFORMATION ON SEQ ID NO. 328:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 140 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GETRVHSQQG GGIKAPSWDW FFREPGPLVK GLLGHVKQYL EQPRPWGYQV ERREGRRLPC 60 THLPWWAGFS LLGSTLPPSV HDTDPRASPC PRPSYRLLFQ DITDNPERME KGGAWVPAVS120 GQKEVACGNL RSPHPRFPKR 140

- (2) INFORMATION ON SEQ ID NO. 329:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

VFPCHLVGAG PTPATTSGTA KGSTRCDYPG PCWQLRIPGT CSDPVSGSSE SQEPRMRALC 60 SPSSKTQGSP PRKGAHVPQR GWLPGCYLFY PTSAAESQGE TASHPKPLGF SREKNLSQKH120 DLFSGCK

- (2) INFORMATION ON SEQ ID NO. 330:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 418 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GSTSTKNTKI SQACGVIVEL IKSKKMAGGA VLLAGPPGTG KTALALAIAQ ELGSKVPFCP 60
MVGSEVYSTE IKKTEVLMEN FRRAIGLRIK ETKEVYEGEV TELTPCETEN PMGGYGKTIS120
HVIIGLKTAK GTKQLKLDPS IFESLQKERV EAGDVIYIEA NSGAVKRQGR CDTYATEFDL180
EAEEYVPLPK GDVHKKKEII QDVTLHDLDV ANARPQGGQD ILSMMGQLMK PKKTEITDKL240
RGEINKVVNK YIDQGIAELV PGVLFVDEVH MLDIECFTYL HRALESSIAP IVIFASNRGN300
CVIRGTEDIT SPHGIPLDLL DRVMIIRTML YTPQEMKQII KIRAQTEGIN ISEEALNHLG360
EIGTKTTLRY SVQLLTPANL LAKINGKDSI EKEHVEEISE LFYDAKSSAK ILGLTRQG 418

- (2) INFORMATION ON SEQ ID NO. 331:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 142 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

VPQCGLGANL PQVVQCLLTD VDSFRLGTDF NDLFHFLWSI QHGPDYHHSV QKVKRDAVRG 60 CDVLSASDDT VASVGCKDDD GSDRRLQGAV QVGEALNVQH VDLINKQHTR DQLSNALVDV120 LVHHLINLPS KFVCDFCLLW LH

- (2) INFORMATION ON SEQ ID NO. 332:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

LAHHGQDILS PLGPRISHIQ VMQGHILDDF FLFVHIPFWQ GDILFSFKVE FCGIGITPAL 60 PLHGPTVGFN VNHISSFYSL FLQTFKNAGV QFQLFGSFGC FESYDHMANG FAISSHGILC120 LTRS

- (2) INFORMATION ON SEQ ID NO. 333:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 176 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

QAMGKKQKNK SEDSTKDDID LDALAAEIEG AGAAKEQEPQ KSKGKKKKEK KKQDFDEDDI 60 LKELEELSLE AQGIKADRET VAVKPTENNE EEFTSKDKKK KGQKGKKQSF DDNDSEELED120 KDSKSKKTAK PKVEMYSGSL TNFLKKLKGK LKNQIRSGMG QRRMRITVKK LKSVQE 176

- (2) INFORMATION ON SEQ ID NO. 334:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 193 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

RFKIKKDCKT ESGNVLWEFN KLPKKAKGKA QKSNKKWDGS EEDEDNSKKI KERSRINSSG 60 ESGDESDEFL QSRKGQKKNQ KNKPGPNIES GNEDDDASFK IKTVAQKKAE KKERERKKRD120 EEKAKLRKLK EKEELETGKK DQSKQKESQR KFEEETVKSK VTVDTGVIPA SEEKAETPTA180 AEDDNEGDKK NER

- (2) INFORMATION ON SEQ ID NO. 335:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 118 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

ETVAFARPFF PSLFSFPPLS SFLFLLIFRS FCLLHCHLLQ LWESLLSLQR QELLQYQQSL 60 WILOFLLQIS FEIPFVYSDP FYLFLTLLFL SASAVSLFLH LAFFSRAPSF LPSFGPLS 118

- (2) INFORMATION ON SEQ ID NO. 336:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 230 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

LQRLLPPGAE RPAHLCTGPG GEDGAGGRVP GTRPQRPPAL QRAEDGRQGG LRVAGTAGPP 60
PGVPLRPGQG GSGHQEQGAS HPGSLDQGLT GAKRPQGCPA CGRRPPCVGG VPGSAHRPQP120
EGAALRGRS RLQQAGPCCC RVLWLRRCHP AGLPRRPPAA DPGARAAAGG RHVLCRSPLH180
PGLRPPLPQW GLLRPEGGCL CVPVSRGILR TALREGAGGE VSGGRGYLGL 230

- (2) INFORMATION ON SEQ ID NO. 337:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 416 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

QDGSGPFLAD FNGFSHLELR GLHTFARDLG EKMALEVVFL ARGPSGLLLY NGQKTDGKGD 60
FVSLALRDRR LEFRYDLGKG AAVIRSREPV TLGAWTRVSL ERNGRKGALR VGDGPRVLGE120
SPVPHTVLNL KEPLYVGGAP DFSKLARAAA VSSGFDGAIQ LVSLGGRQLL TPEHVLRQVD180
VTSFAGHPCT RASGHPCLNG ASCVPREAAY VCLCPGGFSG PHCEKGLVEK SAGDVDTLAF240
DGRTFVEYLN AVTESEKALQ SNHFELSLRT EATQGLVLWS GKATERADYV ALAIVDGHLQ300
LSYNLGSQPV VLRSTVPVNT NRWLRVVAHR EQREGSLQVG NEAPVTGSSP LGATQLDTDG360
ALWLGGLPEL PVGPALPKAY GTGFVGCLRD VVVGRHPLHL LEDAVTKPEL RPCPTP 416

- (2) INFORMATION ON SEQ ID NO. 338:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 241 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

NQHMKNTAMA RPRYPGRRQR STPSHSELLS IAPRRAWGVA EGYGHVQGGW AGPAEGQDTQ 60
IGPGLASAPQ QPGLAQAARE QRRAVPSSNI VWKSQYWRRR PRQGPEHTQE GAAQIGAWKG120
PVGSPGGRAP SDLSSPFLSG TRVPPDGARV IQEPGLLPGG DTVGQAQCKA GAQHLEAGVC180
VLRLPSTPSP PRCHLACPSL STRSVCSTAA WTEGRPGQQS LRPTLRQENH IKKRQVYKNR240
K

- (2) INFORMATION ON SEQ ID NO. 339:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 79 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

LLQPQGEMPP GNPPMSTRGQ EATVLRTPEN LAGELFLVHP SLQLYLCPAD NVKDWSKVVL60 AYEPVWAIGT GKTATPQQG 79

- (2) INFORMATION ON SEQ ID NO. 340:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 62 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

FPVGVLQSCQ YQWPTQAHRP GRPCSSPSRY LQGRDTAGGK GEQERALQPG SPEYEERWPP60 AP

- (2) INFORMATION ON SEQ ID NO. 341:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

SLLGCCSLAS TNGPHRLIGQ DDLAPVLHVI CRAEIQLEGR VNKKELSSQV LRSTKNGGLL60 PPSGHWGISR WHLPLGLEKS 80

- (2) INFORMATION ON SEQ ID NO. 345:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 257 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

KNLSQLEPRE NAKEEVRKER GMGWVAAGAA QLLSLLSTST ASDSSVISSS ACTSGLLPRR 60 RSPASPRSAH LHHLGGLEHF HLALADLLDV EGEGWHLVDR GLGARVHHVV GREGFAQLVP120 RRLQFLAPLG GHQARAQLVH ALLQGVPRLL QVFLGLEARL LQVLAGTHLG LLHLLLGEGL180 LEVVHAPQAL RLIRSARDSS ITSSTSTASS DESSSAAASS SGRSPSPSSS PSFSGSASDS240 FSDLLMLSLA GSFTSSW 257

- (2) INFORMATION ON SEQ ID NO. 346:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 237 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN ·
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

KSRRRCQRRR ARSWARASGP RRTQRRWSFR RTRRWRLRRL LRSPAQSVSS AGPAARGRLQ 60 EGLLQGEDGE DQGAYPREPG EDAPQDQGKP GEDAAHPGEA HEQAGHAPGA RRAARETEDV120 AGQVAQILHA RPRGVRALQD RGLQGATLHL PRQEDPRGPG GSAQGHRDGG GGRSGGRPAT180 CGAGAAPTCT RCWRSPRSRT PCWWTRATAT ERPPLPPTPF LAPSELPLSH SLSARAG 237

- (2) INFORMATION ON SEQ ID NO. 347:
  - (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 263 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GRLPGYPDRR GPGASSAGAQ AAEEPSGAGS EELIKSDQVN GVLVLSLLDK IIGAVDQIQL 60
TQAQLEERQA EMEGAVQSIQ GELSKLGKAH ATTSNTVSKL LEKVRKVSVN VKTVRGSLER120
QAGQIKKLEV NEAELLRRRN FKVMIYQDEV KLPAKLSISK SLKESEALPE KEGEELGEGE180
RPEEDAAALE LSSDEAVEVE EVIEESRAER IKRRACGAWT TSRRPSPRRR WRRPRCVPAR240
TWRRRASRPR KTWRRRGTPW RSA

- (2) INFORMATION ON SEQ ID NO. 348:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

SSGSSRFGSS GSRRRYASLY FCCAIEDQDN ELITLEIIHR YVELLDKYFG SVCELDIIFN 60 FEKAYFILDE FLLGGEVQET SKKNVLKAIE QADLLQEEAE TPRSGS 106

- (2) INFORMATION ON SEQ ID NO. 349:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 78 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

LFLMPQNKVR MVICQEFFIT VSYKKRVALF TVLCVKSLFK ARMFPLGYLL KLNLFCFPPL60 RSAAHFTAAS FLSMALPS 78

- (2) INFORMATION ON SEQ ID NO. 350:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 65 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TCLHGLYFHL YMLGWIKLCC DCDQHSGHVS TVLSHRQLVV INVQRTKKKK GAASLGGITG60 SGVKR

- (2) INFORMATION ON SEQ ID NO. 351:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 196 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

LPGLPLRQLG GVCHGHRPGL LLHQQHGGGA GAVQQPQREE EALHDPGQGS APAELCQFQQ 60 HVPRFPLQQP QAVQEGGAG AGQGLVLWQP GAGLQGVQPG DDGAPDLQHG DAAGDSHHDD120 PAQELPAAEH RAQGPGGPRP ALRGGARSNC RVCLVQMCPE APEGSHQLMP ASDPQQGWFA180 AAAQGEPVSD PGHHHH

## (2) INFORMATION ON SEQ ID NO. 352:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 361 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

SLASLSDSLG VSVMATDQDS YSTSSTEEL EQFSSPSVKK KPSMILGKAR HRLSFASFSS 60
MFHAFLSNNR KLYKKVVELA QDKGSYFGSL VQDYKVYSLE MMARQTSSTE MLQEIRTMMT120
QLKSYLLQST ELKALVDPAL HSEELEAIV ESALYKCVLK PLKEAINSCL HQIHSKDGSL180
QQLKENQLVI LATTTDLGV TTSVPEVPMM EKILQKFTSM HKAYSPEKKI SILLKTCKL1240
YDSMALGNPG KPYGADDFLP VLMYVLARSN LTEMLLNVEY MMELMDPALQ LGEGSYYLTT300
TYGALEHIKS YDKITVTRQL SVEVQDSIHR WERRRTLNKA RASRSSVQPL HLRVVPGARA360
A

## (2) INFORMATION ON SEQ ID NO. 353:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 161 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

VDGFLQGLQD TFVQGRLYNC FELLLGVQGG VHQGLELGAL QQVALELGHH GANLLQHLRA 60 GGLARHHLQA VHLVVLHQAA KVRALVLRQL HHLLVQLAVV GEESVEHAAE TGKAQPVPSL120 AQDHGGLLLH AGAAELLQLL LRAAGGVGVL VGGHDRHPQA V

- (2) INFORMATION ON SEQ ID NO. 354:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 218 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

SGRGPKYVID VEQPFSCTSL DAVVNYFVSH TKKALVPFLL DEDYEKVLGY VEADKENGEN 60 VWVAPSAPGP GPAPCTGGPK PLSPASSQDK LPPLPPLPNQ EENYVTPIGD GPAVDYENQD120 VASSSWPVIL KPKKLPKPPA KLPKPPVGPK PEPKVFNGGL GREAASSVSA QPLLSPQAGL180 GRHGRQSYRR SWEKRRGTGS MVSDTPGTSG LVPGRARW 218

- (2) INFORMATION ON SEQ ID NO. 355:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 253 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

AGEGVDGLTQ ETPLKPVSQL PGPAGAPTGR RGQAEDPGSV MASALRPPRV PKPKGVLPSH 60 YYESFLEKKG PCDRDYKKFW AGLQGLTIYF YNSNRDFQHV EKLNLGAFEK LTDEIPWGSS120 RDPGTHFSLI LRNQEIKFKV ETLECREMWK GFILTVVELR VPTDLTLLPG HLYMMSEVLA180 KEEARRALET PSCFLKVSRL EAQLLLERYP ECGNLLLRPS GDGADGVGHH AADAQRDARG240 PALQGEAGGA PST

(2) INFORMATION ON SEQ ID NO. 356:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 118 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

LTTASREVQE NGCSTSITYL GPLPLHLVMP DHVRPVVHLP RGDRHRRRRP RWAAAAGSRT 60 RGSAPGAVVP PAGSPSGSTR VSPVHGAPPL WPRLQTSCIG AQEAGSSRSG HGAPPPLR 118

- (2) INFORMATION ON SEQ ID NO. 357:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 223 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

DHTCGCAGNL QEAIMLRSGV TSQGIHPGSP WCCTPTQAEL IVGDQSGAIH IWDLKTDHNE 60 QLIPEPEVSI TSAHIDPDAS YMAAVNSTGN CYVWNLTGGI GDEVTQLIPK TKIPAHTRYA120 LQCRFSPDST LLATCSADQT CKIWRTSNFS LMTELSIKSG NPGESSRGWM WGCAFSGDSQ180 YIVTASSDNL ARLWCVETGE IKREYGGHQK AVVCLAFNDS VLG 223

- (2) INFORMATION ON SEQ ID NO. 358:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 193 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

FFFFFFFFF EQHLRVGLLL LPPRLSPRPG PAWPVPNPVG WPGHLHQGQ LLAGTNKPFH 60 LAMVVVFSMD RGPETRAGRG REHTSLGVGT SLRPLSSFGP SADFPRQCRL AQSRSVQPGL120 GRALSHLDKQ LGAESPRAAW PSRSRRHRGP SGPVAQAGRG GSALTWVLHG SLQLPPPAPG180 SPEGSQASPA HCH

- (2) INFORMATION ON SEQ ID NO. 359:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 251 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

PGCCMGPSSC HHLHQAVPRG HRLAQHTVIE GQADNSLLVA AILSLDLSSL HTPEPGQVVR 60
GSSDDVLGVP REGAAPHPAA GGLPGVAALD AQLRHQGEVG RPPDLARLIS RAGGEERGVG120
AEATLQGVAR VGRDLSLGDE LGHLVTNAPR QIPDIAVSGA IDSCHVAGVG IDVGGRDGDL180
GLRDQLLVVV CFQVPDVDSP ALVTHDELCL GWGAAPGTPR VNALGGHTGP QHDCFLQVTS240
TSACMILTSS C 251

- (2) INFORMATION ON SEQ ID NO. 360:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 50 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
   (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:
  GNIPHSNLTD ASSPKRIKIV ACTDQENILG RMKYVCLFFF KNKGFWNSGE

50

- (2) INFORMATION ON SEQ ID NO. 361:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 59 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

KGNQLYQGET RALGTMTTRT AFILHHSDCF QSSNDCQATS QMTDNFCCSF LYKMLRQQA 59

- (2) INFORMATION ON SEQ ID NO. 362:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 67 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

DKILLSPRME CSGMIMAHCS LDLPGSHLSL PSSWDHRHVP PCPANFYFGR DKVSPCCLGR60 FQTPGLK

- (2) INFORMATION ON SEQ ID NO. 363:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 84 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

MRRCIHPSHS LSGSRQTQSP LSHSASNGST TKVAQQMRRA AAVVGESTEE TRLGRALGAA60 GFTNKQLSEN TAQGEEKRVM CLQN 84

- (2) INFORMATION ON SEQ ID NO. 364:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

CAYRTEKWKS HTVPCSPEVK LVLTLALRAF SSMEPLGLGR KARVSAHRHT SYLQDIDGLC 60 RGSTGQPTAN TAASLVSASL LPVHPGDYSW INLPKNSAFI MSLFCSKTQN GSLPPRGRPS120 HHCIPNR 127

- (2) INFORMATION ON SEQ ID NO. 365:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 114 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

	(A)	ORGA	NISM:	HUMAN
--	-----	------	-------	-------

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

PYVHSPAWSP WGLVGRLVSV HTDIPATFRT LIVSAEVALG SQLQTQQPPW FQLLSFQYIL 60 ETTPGLIFLR TQHSLCHFSV RKPKMAPCHL EADQVITVSP TASTVCIWYI VQAP 114

- (2) INFORMATION ON SEQ ID NO. 366:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 30 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

NLHSNIKVFF YNVPKISGPQ QAVFVPVFFN

30

- (2) INFORMATION ON SEQ ID NO. 367:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 44 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

KECMSEAQFL ATTLTKGNNC RGILQLIHTQ HLLHTVFTDS NLVG

44

- (2) INFORMATION ON SEQ ID NO. 368:
  - (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 34 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

NVDFRCKNML EIRFSAIKPN TKKIKKNVCQ KPNS

34

- (2) INFORMATION ON SEQ ID NO. 369:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

QPSSLLHHCP YPYPPRHLLA TPLLKPQLLA GSPAHASLIS FLASPQRASR QHGGPSQRAG 60 TLSCPLVELG GSSGGRGLCH GSADPTNRAA EPQERGEPAA GDRRPLPEWG RVSLAESPGA120 EFRCPGSLGE WGEIPEKESS AHPKTEE

- (2) INFORMATION ON SEQ ID NO. 370:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 244 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

NHSCWQGPQL MPASSPFLLA PKGPPGNMGG PVREPALSVA LWLSWGAALG AVACAMALLT 60
QQTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS RKRRAVLTQK120
QKNDSDVTEV MWQPALRRGR GLQAQGYGVR IQDAGVYLLY SQVLFQDVTF TMGQVVSREG180
QGRQETLFRC IRSMPSHPDR AYNSCYSAGV FHLHQGDILS VIIPRARAKL NLSPHGTFLG240
FVKL

- (2) INFORMATION ON SEQ ID NO. 371:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 185 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

TPASWIRTPY PWACRPLPRL RAGCHITSVT SESFFCFWVS TALLFRDLSP LSQASRASEL 60 CSGRLCQGYP SPFWEGPPVP CSRLTSLLRL CSSVCWVSRA MAQATAPRAA PQLNQRATES120 AGSLTGPPML PGGPLGASKK GDEAGMSWGP CQQLWFQEWG SKEVAGRVRV RAVVQKGRRL180 LRKEK

- (2) INFORMATION ON SEQ ID NO. 372:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 148 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

VLYHCASRYR RRARQTCAPS YTRSADLPSR TPPVEDLLEL SRAFWVGADG GGRVRVLGGT 60 EAHEDGIPPE SMDHYADGHR PQHCHLGYRC HGRPQREGLP RCLKVPPVNL SSVSVPFPVT120 HRAGMEFNGC SGQTLVHGQT SLLWILQD

- (2) INFORMATION ON SEQ ID NO. 373:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 135 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CLPVRRLRQF EPKTPKVEAE FQSMGSRLSQ PFESYITAPP GTAAAPAKPA PPATPGAPTS 60 PAEHRLLKTC WSCRVLSGLG LMGAGGYVYW VARKPMKMGY PPSPWTITQM VIGLSIATWG120 IVVMADPKGK AYRVV 135

- (2) INFORMATION ON SEQ ID NO. 374:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 152 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

IPCLLCVSRG KGQRQKTDSL VVLSNNAVGL PFGVCHDNDT PGGNAEADDH LRNGPWTRGV 60 SHLHGLPCHP VHVPARPHQP QPRKHATAPA GLQQAVFCWG GRRSGCSWGR RFGGRGGTG120 RRSDIGLKRL GQPRPHALEL GLNLGRLWFK LA 152

- (2) INFORMATION ON SEQ ID NO. 375:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 107 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GAELQLRSCA MAVSQEGLDG EVKAPDARIF IPCANTAFTP DLQVLQQVLS SFTVSSPLFH 60 SGFICYTPNL FSQSTPQSLP CWGQHRKRQN LRKEKGNLQP AMDLMIP 107

- (2) INFORMATION ON SEQ ID NO. 376:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 113 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

IPKNFYHNIH RSLYQLYLEV KQAWESIDCS ACPRVEALNK ATKTPEITDL TFQWPTGPGS 60 GQVGHQANHL FPCASLCKSW SVPLARPSLV QDLGPQTKES RGLGFPDPRM VSL 113

- (2) INFORMATION ON SEQ ID NO. 377:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

FGGPQAQPHS AVGSSLSSQI QVNLSFKNKG EPQTCSTTRD NNTPWQEDHV LDCLRTATVR 60 QEACCDPLCS MPIAQASSIP YHLPPMLFFG TTTLAKREYG KQRPRALLQY RHFEVGRQHM120 LHSK

- (2) INFORMATION ON SEQ ID NO. 378:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 66 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

HKIILISRYR RNSVVTCQAI LYTPMILQRK HPSLLLPLLW QLKCICSSTL KRRKRNNLSL60 IPKLPH

- (2) INFORMATION ON SEQ ID NO. 379:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 67 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

PEKSPGAGPL LGGSPFFFFF YVSKSTEFIL KHSIKFESHE TKASLHYMLI LAKSKDQHTI60 DIHDNVV 67

- (2) INFORMATION ON SEQ ID NO. 380:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

FCIHFECLHV KTQLIYYFNI KPISFEAKLI LLFYKSNGDS FFRMLKAQCL RFMLAALLAL60 LLPEMKTKQN R 71

- (2) INFORMATION ON SEQ ID NO. 381:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 107 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

MDGAQGRLLP VSSRHSNLAL LKPTSRDLTA PPEGASLMTV GGITAPRDVQ VWNPRTWESV 60 TLRGKRDPAP VLQFRISWWG DDRGWLRWAL SNHGGPYKGR GVTRVCA 107

- (2) INFORMATION ON SEQ ID NO. 382:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 143 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

EVENHTNLLS YSSRGQESKM VFTRLKSCQC GFVSPRRLWG RIQCLFQLLQ GPPHRLAPGL 60 LAIFTARSFL ASCADPRDSP SLIRAPMITQ GPPQPSTVIS PPRNPELKHR RRVPFATQGN120 TFPRFGVPNL DISGGCYSTH RHQ 143

- (2) INFORMATION ON SEQ ID NO. 383:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

SHTHAQLSNH GGVQEPPLPL GVPKPWGSDS GALSRPGCKL KTPGGFQNAQ CLGHNLDQLN60 LNLQRDITAP QETPRGSQSA KPEETI 86

- (2) INFORMATION ON SEQ ID NO. 384:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

LEPIRFQQKV MEKETEKRIS EIEDAAFLAR EKAKQDAEYY AAHKYATSNK HKLTPEYLEL 60 KKYQAIASNS KIYFGSNIPN MFVDSSCALK YSDIRTGRES SLPSKEALEP SGENVIQNKE120 STG

- (2) INFORMATION ON SEQ ID NO. 385:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 83 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

DNSCVRYVEA QQKSHGTTSR NLSAVRPVSL MTVCWLCQTL YLGKESPDLN GSFPWALSYR60 GICNMEKIIF HFCSFNSINS LYK

- (2) INFORMATION ON SEQ ID NO. 386:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 88 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CLTFQCRQYL SIRLSSFMSS SLERNTYRIL DKTVAEKTIC VSDSWLYPPI SGAPRTIAGE60 VEQMKCKFSV NLKSPYNDCS HLTPWATS 88

- (2) INFORMATION ON SEQ ID NO. 387:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 105 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
   (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60 RDLLLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

- (2) INFORMATION ON SEQ ID NO. 388:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 173 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AQESPWQLCR GARTSKRKLP KLGMEQHCNE MCPPSSLFLP GAYKAQMYSD VWTNTKKKKK 60 KKKKKAFLSH RHKTQIIYCY EALFTNGQFL HFIAACERLP DGRPISLVLQ TSSQAAFYQK120 GENSCLSFLK NAFLYLSIRH YTSELYKRPG GTMSLVDTFH CSVAPFLAWE ASA 173

- (2) INFORMATION ON SEQ ID NO. 389:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 105 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60 RDLLLLARLO GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

- (2) INFORMATION ON SEQ ID NO. 390:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 262 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

RCPRRGREMD SGCWLFGGEF EDSVFEERPE RRSGPPASYC AKLCEPQWFY EETESSDDVE 60
VLTLKKFKGD LAYRRQEYQK ALQEYSSISE KLSSTNFAMK RDVQEGQARC LAHLGRHMEA120
LEIAANLENK ATNTDHLTTV LYLQLAICSS LQNLEKTIFC LQKLISLHPF NPWNWGKLAE180
AYLNLGPALS AALASSQKQH SFTSSDKTIK SFFPHSGKDC LLCFPETLPE SSLIFCGRDT240
RNGRKIGKFC KCANLVGERG TG 262

- (2) INFORMATION ON SEQ ID NO. 391:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 66 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

KPVPLSPTRL AHLQNFPIFL PFLVSLPQKI KELSGKVSGK HKRQSFPECG KKDLIVLSLE60 VKLCCF

- (2) INFORMATION ON SEQ ID NO. 392:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 78 amino acids
      - (B) TYPE: Protein
      - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

QAGGRVPWLN GLCWLLYFPS LQQSPAPPYA YPGEPDTEPD LPGHPFSWQN WLMTIFQRYW60 NTPAVLSDTL VVCRPGLL 78

- (2) INFORMATION ON SEQ ID NO. 393:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 79 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

TSLEGIDLOP SHLTIYTAAL KEKTPDFRRL SPRVSETADS RKVARGPRFV MRDNPGRGGD60 HRGLQAPGWM KEGRGWGVL 79

- (2) INFORMATION ON SEQ ID NO. 394:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 72 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

VTPPPPSQIS SFLPPSTAPF TKPPIPDPPS STPAPGDPYD HPRARGCPAL QIGAHGRPYG60 SPRSPRREER DV 72

- (2) INFORMATION ON SEQ ID NO. 395:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 98 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

PPPPPPKFHP SFRLLQPPLQ NPPSPTLLHP PRRLETPMIT PAPGVVPHYK SGPTGDLTGV60 RGLRDARRET SEVWRLFLQG CCVDCEVGGL KINSLEGG 98

- (2) INFORMATION ON SEQ ID NO. 396:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

NWRQTVWQRV REGACAQESS RPASGCRFLR CAIGASAFSG DRGSAVATNT QPHTHNHTHK60 WGQPHPVQAF TNVISVLFYF 80

- (2) INFORMATION ON SEQ ID NO. 397:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 309 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

YDNSSTCKKG KVFPGKISVT VSETFDPEK HSMAYQDLHS EITSLFKDVF GTSVYGQTVI 60 LTVSTSLSPR SEMRADDKFV NVTIVTILAE TTSDNEKTVT EKINKAIRSS SSNFLNYDLT120 LRCDYYGCNQ TADDCLNGLA CDCKSDLQRP NPQSPFCVAS SLKCPDACNA QHKQCLIKKS180 GGAPECACVP GYQEDANGNC QKCAFGYSGL DCKDKFQLIL TIVGTIAGIV ILSMIIALIV240 TARSNNKTKH IEEENLIDED FQNLKLRSTG FTNLGAEGSV FPKVRITASR DSQMQNFYSR300 HSSMPRPDY

- (2) INFORMATION ON SEQ ID NO. 398:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 105 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEOUENCE DESCRIPTION: SEO ID NO: 398:

QALIASTIFN VIDSYLASEL DSLQTFTTSI QRGWQMSDGR KTPEARSLLV LTSPSVFLNT 60 LNNSLYIGWG PWRVPHSYDS NSQGGACCCV LNRDFASGCL WRPLS 105

- (2) INFORMATION ON SEQ ID NO. 399:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

CFSCFVICSV SLCTLNIYPL CDKKKKKKK SRTSTFDFSQ PQPRKNGSWD KQLVFVSKTQ60 IGHINATAFR SFDFD 75

- (2) INFORMATION ON SEQ ID NO. 400:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 70 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

RKKAVCFMND LICFLDNTFK NNVLSQAWWC VHLVPTIWEA EAGGSLEPRS LKLQCPVVAP60 VNNCTPAWAT

- (2) INFORMATION ON SEQ ID NO. 401:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 69 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

LVPQGSLLQT HPFVFFSFLE MRSRYVAQAG VQLFTGATTG HCSFKLLGSS DPPASASQIV60

GTRCTHHHA

69 ......

- (2) INFORMATION ON SEQ ID NO. 402:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

PPLWVATVRN GCCHVFWTLP ANRSLPGFGN TSITSLLLFC RDKTFEVARP RTSKDSCYSA60
TVYTAHLSYS HVLSSLVRLF 80

- (2) INFORMATION ON SEQ ID NO. 403:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 81 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

LTNMSDHLFG WLLLEMAVVM FSGLCQPTDP CQVLEILLLP RCYFSAGIKL LRWPDPEHPR60 IPVTVLQYTL LIYPILMCFL L 81

- (2) INFORMATION ON SEQ ID NO. 404:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

VSHYPHSVSK PPKHQTKQMV VALTHSRLTS EFKWENTPYT TVIIPLWTLN ITYFLKIILL60 KKKAHENRIN EQCIL 75

(2) INFORMATION ON SEQ ID NO. 405:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 328 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

RYLNMGNLLK VLTCTDLEQG PNFFLDFENA QPTESEKEIY NQVNVVLKDA EGILEDLQSY 60 RGAGHEIREA IQHPADEKLQ EKAWGAVVPL VGKLKKFYEF SQRLEAALRG LLGALTSTPY120 SPTQHLEREQ ALAKQFAEIL HFTLRFDELK MTNPAIQNDF SYYRRTLSRM RINNVPAEGE180 NEVNNELANR MSLFYAEATP MLKTLSDATT KFVSENKNLP IENTTDCLST MASVCRVMLE240 TPEYRSRFTN EETVSFCLRV MVGVIILYDH VHPVGAFAKT SKIDMKGCIK VLKDQPPNSV300 EGLLNALRYT TKHLNDETTS KQIKSMLQ

- (2) INFORMATION ON SEQ ID NO. 406:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 115 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

YYIHLIINFL LRLCRLGIFK IKEKIWPLLK VCACQNFKKI PHVKVPSASA GDSVLVLLSS 60 ARASRRSQSR SCALLDRRGG SSAALGGAPG PERGSGGSRT GSPSTPAPVA EPPQA

- (2) INFORMATION ON SEQ ID NO. 407:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 100 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

QEPALALDAG WENMGYLLRL PEDLLMLLLT SEKIRKISLI CLLVEQLHPM PSLATSHLLD 60 AGLPLVFRGQ LLCMTASPPR CLLHLILHS PDYKFPSQTL 100

- (2) INFORMATION ON SEQ ID NO. 408:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 116 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

TVLHSHLPSS CLPCLSTHSV KEPRGATSPR LCFPTACGMG VSSATAGLRC FHQPCRHLVL 60 HEEQTLRGWS GMGRSPLGGQ ALVPSRFPSL APGVHTAQSA PGGWKPPCFR SLGSPP 116

- (2) INFORMATION ON SEQ ID NO. 409:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 132 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

SPDERCSIRT SPPRACPASP RTVLRSQEEP LRPDFVSPPP AAWVCPVPPL ASAASISLVA 60 TWSFMKSRHL EAGREWGGRP WEGRRWFQAG SRPWRLECTQ PSRHLVAGSH PALDHSGPHL120 RRVPALDQSR GH

- (2) INFORMATION ON SEQ ID NO. 410:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 142 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

WKQRRPAVAL DTPMPQAVGK QSLGEVAPLG SLTLCVERQG RHEEGRCEWS TVHPGISQPE 60 SPPSLAAPEH SLWPTATEMS ACQDTWRKK TRHQKKLPPQ EQIELLDQGH TRSGRHPAPC120 AQGKETQFNV WLLCSRETAT LP

- (2) INFORMATION ON SEQ ID NO. 411:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 244 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

KRRGVRQFRW LVCTRRASPG AARSAPIAPA TGSGRRPNMD SAGQDINLNS PNKGLLSDSM 60 TDVPVDTGVA ARTPAVEGLT EAEEEELRAE LTKVEEEIVT LRQVLAAKER HCGELKRRLG120 LSTLGELKQN LSRSWHDVQV SSAYVKTSEK LGEWNEKVTQ SDLYKKTQET LSQAGQKTSA180 ALSTVGSAIS RKLGDMRNSA TFKSFEDRVG TIKSKVVGDR ENGSDNLPSS AGSGDKPLSD240 PAPF

- (2) INFORMATION ON SEQ ID NO. 412:
  - (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 149 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

LGHFLIPLSK FLRSFHIGAR DLHVMPAPGQ VLFQLPQGGE AQPPLELSTV PLLGCQDLAQ 60 SDNFLFHLGK LSPELLLLSL CQTLNSRSPG SHTCVDRNIR HGVRQQTFVR RIQVDILAGG120 VHVRAASGPC RGRYGSRAGG AGRSSPRTH

- (2) INFORMATION ON SEQ ID NO. 413:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 143 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

ALETCTSCQL LDRFCFSSPR VERPSLLLSS PQCLSLAART WRRVTISSST LVSSALSSSS 60 SASVRPSTAG VRAATPVSTG TSVMESDSRP LLGEFRLISW PAESMFGRRP DPVAGAMGAE120 RAAPGEARRV HTSQRNCLTP RRF

- (2) INFORMATION ON SEQ ID NO. 414:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 105 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

RGRGALWWAA KELRRTKKLS DYVGKNEKTK IIAKIQQRGQ GAPAREPIIS SEEQKQLMLY 60 YHRRQEELKR LEENDDDAYL NSPWADNTAL KRHFHGVKDI KWRPR 105

- (2) INFORMATION ON SEQ ID NO. 415:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 386 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

AAELRDCGSR RISRSPSSNS HLSPRISLSG NLGPQTSRLG GPPSPSATWS VFWQLPRQQS 60
LPGRGSANLL PSVRSESAVL SDCVGGFPGR SSVRAWIAGP RCTPASPTRV LSLSWRLFNS120
ASLLLLATST SGSECRFPRS PRARERGIPD CERLLVRRSC WRSGDPRPAG PAGHAAGAFS180
TPQYLGGTAM VLLHVKRGDE SQFLLQAPGS TELEELTVQV ARVYNGRLKV QRLCSEMEEL240
AEHGIFLPPN MQGLTDDQIE ELKLKDEWGE KCVPSGGAVF KKDDIGRRNG QAPNEKMKQV300
LKKTIEEAKA IISKKQVEAG VCVTMEMVKD ALDQLRGAVM IVYPMGLPPY DPIRMEFENK360
EDLSGTQAGL NVIKEAEAHC GGQPRS

- (2) INFORMATION ON SEQ ID NO. 416:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 182 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GVEKAPAAWP AGPAGRGSPD RQQLRRTNSR SQSGIPRSLA RGERGKRHSL PEVDVAKSNS 60 EAELKSRQLK LRTRVGEAGV HRGPAIQART ELRPGKPPTQ SERTADSERT DGRRFADPLP120 GSDCCRGNCQ NTDQVAEGEG GPPNRLVWGP RFPLREIRGL RWELLDGERE IRREPQSRSS180 AA

- (2) INFORMATION ON SEQ ID NO. 417:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 467 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

HTLSRWTKHS IPRWNDARTD DTWHSELDMR KIGQARNTLM DMRLSQVSDS VSGQTVVDPK 60
GYLTDLNSMI PTHGGDINDI KKARLLLKSV RETNPHHPPA WIASARLEEV TGKLQVARNL120
IMKGTEMCPK SEDVWLEAAR LQPGDTAKAV VAQAVRHLPQ SVRIYIRAAE LETDIRAKKR180
VLRKALEHVP NSVRLWKAAV ELEEPEDARI MLSRAVECCP TSVELWLALA RLETYENARK240
VLNKARENIP TDRHIWITAA KLEEANGNTQ MVEKIIDRAI TSLRANGVEI NREQWIQDAE300
ECDRAGSVAT CQAVMRAVIG IGIEEEDRKH TWMEDADSCV AHNALECARA IYAYALQVFP360
SKKSVWLRAA YFEKNHGTRE SLEALLQRAV AHCPKAEVLW LMGAKSKWLA GDVPAARSIL420
ALAFQANPNS EEIWLAAVKL ESENDEYERA RRLLAKARTV PPPPGCS

- (2) INFORMATION ON SEQ ID NO. 418:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 352 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

TPGRWGHCPR LGQQPPGPLV LIILGLQLHG CQPDLLTVGV GLEGQGQDAP CCRHIPCQPL 60
GLGAHEPQHL CFGAVGHSPL QECFQGLPSA MVLLEVRGAQ PHTLLAGEHL QGVGVDGSCT120
LQGIVGYTTV SILHPGMLPI FLLNPNPNHG THDGLAGGHT PSPVTFLGIL DPLLTVDLHT180
VGPQRGDGSV DDLLHHLRVP IGFLQLSSRD PDMSVCRNVL PRLVQDLAGI FIGLQPCQSK240
PELHAGGAAL HSSAQHDSSI FRFFQLNGCF PQANRVWNML EGFPKNPLLC TNVRFQLCGS300
DVNPDRLWEM TDSLGYHGLG CVPRLQPGCF QPDIFTLGAH LRPLHDKVPS YL 352

- (2) INFORMATION ON SEQ ID NO. 419:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 424 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

PPGAPFFLFF FFLTRDIKTF NEGGHSSEPF HMRPNPAPRR PAMATAQSEG VLDAAGHQPK 60
DVPDLLLPVG DVLGHGAPQL PMPRLCTLTA LPHLLLLLS AMLQLKLVEE GPGIPQVRVN120
LHSAVEPLPG LGDLPLTPKQ LGHGQEHMGV MLTLLQGIHA LGPPLGPCLE EDGLRPQDTG180
VGALLQRLGH ECICDVLQPR TVLQPHGLQP QPRVLWVLQT RLFQNGPCSS KLPNLLLQPR240
EQKPQGCGVG TLLQPLVIGF PRLLHHLLLL LDLPLHHPQL GEVLIVPQGL LAQILGCPDV300
VLHPLQLHRL HEHPGGGGTV RALASSLRAR SYSSFSDSSF TAASQISSLL GLAWKARAPM360
LLAAGTSPAS HLDLAPMSHS TSALGQWATA LCRSASRDSR VPWFFSKYAA RSHTLFLLGN420
TCRA

- (2) INFORMATION ON SEQ ID NO. 420:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 109 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GRTLPRGGGT VWVQGHGLEG WWAALSGSGF PAVGFLFWLL RLVYFLSLLP VTPGAPEYRL 60 FSPWAVSLSC FLTLLPGLLC VHLRLAWSKQ VRPLLLYSLV LFWHLVKLA 109

- (2) INFORMATION ON SEQ ID NO. 421:
  - (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 177 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

VSVPSSSAAG TLFQGLCGAP DAPHPLSKIP GGRGGGRDPS LSALIYKDEK LTVTQDLPVN 60 DGKPHIVHFQ YEVTEVKVSS WDAVLSSQSL FVEIPDGLLA DGSKEGLLAL LEFAEEKMKV120 NYVFICFRKG REDRAPLLKT FSFLGFEIVR PGHPCVPSRP DVMFMVYPLD QNLSDED 177

- (2) INFORMATION ON SEQ ID NO. 422:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 114 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

ASRPYILELR EKDPCRPLAH RGSSTVGEGH QEHHRGPGTM CLQHWSWGHL LNGKILLSWV 60 FIILGGSAQG GRRRGEWVG GRVGGCGVAR AGRSLWAKSL SGRGRVPSSC LSER 114

- (2) INFORMATION ON SEQ ID NO. 426:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 50 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

50

	PFCSSI	LAKLQ (	giwgmw	DLQF !	₽Æ
	(2)	INFO	RMATIO	ON ON	ſ
work, dust their		(i)	(B) (C)	ENCE LENG TYPE STRA TOPC	T :: :N
n i		1223		DOLL	17

(vi)	ORIGIN		
	(A)	ORGANISM:	HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

APASALSOV LTPAPASAPA PGRAPAPAAA

SEQ ID NO. 427:

- CHARACTERISTIC:
  - TH: 114 amino acids
  - Protein
  - ND: individual
  - LOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427: EDKMRPGLSF LLALLFFLGQ AAGDLGDVGP PIPSPGFSSF PGVDSSSSFS SSSRSGSSSS 60 RSLGSGGSVS QLFSNFTGSV DDRGTCQCSV SLPDNNFPVD RVERWNSQLI VISQ 114
- (2) INFORMATION ON SEQ ID NO. 428:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 113 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

EITMSCEFOR STLSTGKLLS GRETEHWQVP RSSTEPVKLE NNWDTEPPLP KLRLELEPDL 60 ELELKLELES TPGKELKPGL GIGGPTSPKS PAAWPRKNRR ARRNERPGLI LSS

- (2) INFORMATION ON SEQ ID NO. 429:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 50 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AAAGAGARPG AGAEAGAGVN TWERAEAGAG NWRSHIPQIP CSLAKEEQKG

50

- (2) INFORMATION ON SEQ ID NO. 430:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 224 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

QTQKVVTSPP RITLHWLLPC AAHPPDLHKK GQENSGCAPA TAHSAPPGRS PPELRAGLQR 60 LARAVLPVSR FSAPQPPAAS FSGPRVAPSE ESGPGTSSNS GRLALPRLRS LCPLGVARPR120 CCRALARCCC SSSPRTAAWA RRAGSSSLAS PTSPTSAELQ AHPGQPAAVP RHRIPEHAAA180 QPAGPRDHEG GAGAGRRLDP AGHEAVPPGH QEVPVLALRP RLPR 224

- (2) INFORMATION ON SEQ ID NO. 431:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 408 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

PALLGLPFIG SSLAPPTLQI CIKKAKKTLA VPQQRLILLP RVGAPRSCAR ACSASPALSS 60 RCPASPRPSR RLPAFRGPES HPAKRAGPGQ ARTPAASPFP GSAPSAPSGS RAHDAAGPWL120 AAAALPRLAL LPGLGARALP LWPARLLQA QNCKPIPANL QLCHGIEYQN MRLPNLLGHE180 TMKEVLEQAG AWIPLVMKQC HPDTKKFLCS LFAPVCLDDL DETIQPCHSL CVQVKDRCAP240 VMSAFGFPWP DMLECDRFPQ DNDLCIPLAS SDHLLPATEE APKVCEACKN KNDDDNDIME300 TLCKNDFALK IKVKEITYIN RDTKIILETK SKTIYKLNGV SERDLKKSVL WLKDSLQCTC360 EEMNDINAPY LVMGQKQGGE LVITSVKRWQ KGQREFKRIS RSIRKLQC 408

- (2) INFORMATION ON SEQ ID NO. 432:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 323 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

VISFTFIFSA KSFLQSVSIM SLSSSFLFLQ ASHTFGASSV AGRRWSLLAR GMQRSLSWGK 60
RSHSSMSQQG KPKADMTGAQ RSFTCTQSEW HGWMVSSRSS RQTGAKSEHR NFLVSGWHCF120
MTSGIQAPAC SSTSFMVSWP SRLGSRMFWY SMPWHSCRLA GMGLQFCACR RSRAGQRGRA180
RAPSPGSSAR RGRAAAASQG PAASWARDPE GAEGAEPGKG EAAGVRACPG PALFAGCDSG240
PRKAGSRRLG RGEAGHREDS AGEALQARAQ LRGAPTRGSR MSRCWGTARV FLAFFMQIWR300
VGGAREEPMK GNPRRAGHYF LGL 323

- (2) INFORMATION ON SEQ ID NO. 433:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 333 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

RGRTWELFLA GRRVLVTGAG KGIGRGTVQA LHATGARVVA VSRTQADLDS LVRECPGIEP 60
VCVDLGDWEA TERALGSVGP VDLRGDCADM ELFLAGRRVL VTGAGKGIGR GTVQALHATG120
ARVVAVSRTQ ADLDSLVREC PGIEPVCVDL GDWEATERAL GSVGPVDLLV NNAAVALLQP180
FLEVTKEAFD RSFEVNLRAV IQVSQIVARG LIARGVPGAI VNVSSQCSQR AVTNHSVYCS240
TKGALDMLTK VMALELGPHK IRVNAVNPTV VMTSMGQATW SDPHKAKTML NRIPLGKFAE300
VEHVVNAILF LLSDRSGMTT GSTLPVEGGF WAC 3333

- (2) INFORMATION ON SEQ ID NO. 434:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 210 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

APGHNLRHLD DRTQVHLKGS VKGLLGDLQE GLQQGDSGVV HQQVHGAHAA QRPLGGLPVT 60 QVHAHGFYPR ALADKAVKIR LSPAHSHHPR ARRVQRLDRA APYTFACPGD QHPAAREEQL120 HVGAVSAQVH GAHAAQRPLG GLPVTQVHAH GFYPRALADK AVKIRLSPAH SHHPRARRVQ180 RLDRAAPYTF ACPGDQHPAA REEQLPCSPT 210

- (2) INFORMATION ON SEQ ID NO. 435:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 132 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

FFFFFFFFL GSRIRFIGGI GGRMSTAWGL RCVEGAQQAQ KPPSTGKVEP VVMPLRSLSR 60 KRMAFTTCST SANLPSGIRF SIVLALWGSL QVAWPMDVIT TVGFTAFTRI LWGPSSRAIT120 LVSMSRAPLV EQ

- (2) INFORMATION ON SEQ ID NO. 436:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

KAKSWYPSDF RFQELPENTR SQRVIFWSLF CRDSWEYGHP APRCGNESSR SGEAALADVQ60 LAAPVSNQLH PDGVEDRGVG GLLPELHHAE PYLV 94

- (2) INFORMATION ON SEQ ID NO. 437:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 70 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

FSGVCFAGIA GSMATLLHDA VMNPAEVVKQ RLQMYNSQHR SAISCIRTVW RTEGLGAFYR60 SYTTPSPISC

- (2) INFORMATION ON SEQ ID NO. 438:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 98 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

KAPNPSVLHT VRMQLIADRC CELYICKRCF TTSAGFITAS WSRVAILPAI PAKQTPENYP60 LRSGVLRKFL EPKIRRNPGL SFLRSKMYYQ SAQVSTDS 98

- (2) INFORMATION ON SEQ ID NO. 439:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 270 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

RSVVRRCLKM AAEEPQQQKQ EPLGSDSEGV NCLAYDEAIM AQQDRIQQEI AVQNPLVSER 60 LELSVLYKEY AEDDNIYQQK IKDLHKKYSY IRKTRPDGNC FYRAFGFSHL EALLDDSKEL120 QRFKAVSAKS KEDLVSQGFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL180 VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEPM CKESDHIHII ALAQALSVS1240 QVEYMDRGEG GTTNPHIFPE GFRAQGLTLF

- (2) INFORMATION ON SEQ ID NO. 440:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 145 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

RWRRRNLSSR SRSRWAATPK VLTVWPMMKP SWLSRTEFSK RLLCRTLWCQ SGWSSRSYTR 60 SMLKMTTSIN RRSRTSTKST RTSARPGLTA TVSIGLSDSP TWRHCWMTAR SCSGSRLCLP120 RARKTWCPRA SLNSQLRIST TRSWT

- (2) INFORMATION ON SEQ ID NO. 441:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 210 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

IAPSRLKQGK TLGSEALRED VRIGGAALAA VHVLHLDGHA EGLGQRNDVD VVALLAHGLH 60 LLLAELLDSP STLDEVLEEL ALALQVARGE QPQVDHKVVG GALVIEGGQQ VGDRGLLHL120 LNQVHERVVE ILNCEFSEAL GHQVFLALGR HSLEPLQLLA VIQQCLQVGE SESPIETVAV180 RPGLADVRVL FVEVLDLLLI DVVIFSILLV 210

- (2) INFORMATION ON SEQ ID NO. 442:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 322 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

NSERGRLQAM MTHLHVKSTE PKAAPQPLNL VSSVTLSKSA SEASPQSLPH TPTTPTAPLT 60
PVTQGPSVIT TTSMHTVGPI RRRYSDKYNV PISSADIAQN QEFYKNAEVR PPFTYASLIR120
QAILESPEKQ LTLNEIYNWF TRMFAYFRRN AATWKNAVRH NLSLHKCFVR VENVKGAVWT180
VDEVEFQKRR PQKISGNPSL IKNMQSSHAY CTPLNAALQA SMAENSIPLY TTASMGNPTL240
GNLASAIREE LNGAMEHTNS NESDSSPGRS PMQAVHPVHV KEEPLDPEEA EGPLSLVTTA300
NHSPDFDHDR DYEDEPVNED ME

- (2) INFORMATION ON SEQ ID NO. 443:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 103 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

FGTRAPASHD DPPACEVYRT QSCPSAPESG IKCHPLQVRI GGFSTELTSY SNDPNRPPDS 60 RHPRPLCHHN HQHAHGGTHP QAVLRQIQRA HFVSRYCAEP RIL 103

- (2) INFORMATION ON SEQ ID NO. 444:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

SLSWSKSGLW LAVVTKDRGP SASSGSRGSS LTCTGCTACI GDLPGLLSLS LLLVCSIAPF 60 SSSRIALAKL PRVGFPMEAV VYRGILFSAI EACKAALRGV Q 101

- (2) INFORMATION ON SEQ ID NO. 445:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 539 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

LDVQVKDDSR ALTLGALTLP LARLLTAPEL ILDQWFQLSS SGPNSRLYMK LVMRILYLDS 60
SEICFPTVPG CPGAWDVDSE NPQRGSSVDA PPRPCHTTPD SQFGTEHVLR IHVLEAQDLI120
AKDRFLGGLV KGKSDPYVKL KLAGRSFRSH VVREDLNPRW NEVFEVIVTS VPGQELEVEV180
FDKDLDKDDF LGRCKVRLTT VLNSGFLDEW LTLEDVPSGR LHLRLERLTP RPTAAELEEV240
LQVNSLIQTQ KSAELAAALL SIYMERAEDL PLRKGTKHLS PYATLTVGDS SHKTKTISQT300
SAPVWDESAS FLIRKPHTES LELQVRGEGT GVLGSLSLPL SELLVADQLC LDRWFTLSSG360
QGQVLLRAQL GILVSQHSGV EAHSHSYSHS SSSLSEEPEL SGGPPHITSS APELRQRLTH420
VDSPLEAPAG PLGQVKLTLW YYSEERKLVS IVHGCRSLRQ NGRDPPDPYV SLLLLPDKNR480
GTKRRTSQKK RTLSPEFNER FEWELPLDEA QRRKLDVSVK SNSSFMSRER DCWGRCSWT 539

- (2) INFORMATION ON SEQ ID NO. 446:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

LLCLPAFVSL HHRLNVMSLK LGSKGRACAL QPFHLTGPYS GLCLTKEKNR MFPLLHGLYP60 SGPLGRGPEL AVSCFACTLF SLPPNSSGPS VSVPGOWOH

- (2) INFORMATION ON SEQ ID NO. 447:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 112 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

	(XI) SEQUENCE DESCRIPTION. SEQ ID NO. 447.
vw ss	IKLFTCST SSNSAAVGRG VRRSRRKCRR PDGTSSRVSH SSRKPLFKTV VRRTLHLPRK 60 LSKSLSKT STSSSWPGTD VTITSKTSFQ RGLRSSRTTW LRKLRPANFS LT 112
(2) I	NFORMATION ON SEQ ID NO. 451:
(	<ul> <li>(i) SEQUENCE CHARACTERISTIC:         <ul> <li>(A) LENGTH: 56 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> </ul>
	(ii) MOLECULE TYPE: ORF
1	(iii) HYPOTHETICAL: yes
1	(vi) ORIGIN (A) ORGANISM: HUMAN
ı	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:
FFFFFVE	rgf rhvdetglel Lassdlppql lkvlglyrhe plslalkrfs Qrpsvr 56
(2) II	NFORMATION ON SEQ ID NO. 452:
	<ul> <li>(i) SEQUENCE CHARACTERISTIC:         <ul> <li>(A) LENGTH: 56 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> </ul>
	(ii) MOLECULE TYPE: ORF
	(iii) HYPOTHETICAL: yes
	(vi) ORIGIN (A) ORGANISM: HUMAN
e.	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:
IRFGÍS	CPGP GISLQEPLPL CWRHSFRIRR RREKRKCKGG RSFPGRTISV THMDPR 56
(2) I	NFORMATION ON SEQ ID NO. 453:
	<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 57 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- ORIGIN (vi)
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

VTEMVRPGKD LPPLHFLFSL LLLILKLCLQ QRGRGSCREI PGPGQEMPNL IYLTEGL

- (2) INFORMATION ON SEQ ID NO. 454:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 80 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

ILAFWRAAPL WHHQTLLCFP STWNSSNIRG CEGLAILLSW VHVSDRNGAA WERSPSFTFS60 80 LLPPPPYSKT VPPTEGQGLL

- (2) INFORMATION ON SEQ ID NO. 455:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 182 amino acids

    - (B) TYPE: Protein (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

ARLPLLAAED RGQPGSVKDP KMAGRKLALK TIDWVAFAEI IPQNQKAIAS SLKSWNETLT 60 SRLAALPENP PAIDWAYYKA NVAKAGLVDD FEKKFNALKV PVPEDKYTAQ VDAEEKEDVK120 SCAEWVSLSK ARIVEYEKEM EKMKNLIPFD QMTIEDLNEA FPETKLDKKK YPYWPHQPIE180

(2) INFORMATION ON SEQ ID NO. 456:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 76 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:
AQSIAGGFSG KAANLEVRVS FQDFRELAMA FWFWGMISAK ATQSMVFRAS FRPAILGSFT60 DPGCPRSSAA SNGSRA 76
(2) INFORMATION ON SEQ ID NO. 457:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 104 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:
CPECVIQGPE LPPGLNFINS QLVGEANRDT FSCLIWFLGK LHSSPQWSSD QMELSSSSP 60 SLSHILQSWP LRETPTQHKI SHLLFLRHPP GQYIYPLARE PSAH 10
(2) INFORMATION ON SEQ ID NO. 458:
<ul><li>(i) SEQUENCE CHARACTERISTIC:</li><li>(A) LENGTH: 223 amino acids</li><li>(B) TYPE: Protein</li></ul>

- (C) STRAND: individual (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

RGAGGHQGES GRPEGWPPF LHPRGRFQVP WLESVLIVVS NNIDEEALAR LAQEGSEVNV 60
IGIGTSVVTC PQQPSLGGVY KLVAVGGQPR MKLTEDPEKQ TLPGSKAAFR LLGSDGSPLM120
DMLQLAEEPV PQAGQELRVW PPGAQEPCTV RPAQVEPLLR LCLQQGQLCE PLPSLAESRA180
LAQLSLSRLS PEHRRLRSPA QYQVVLSERL QALVNSLCAG QSP 223

- (2) INFORMATION ON SEQ ID NO. 459:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 157 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

VIRVVSSQPR SESQGDCPAH RLFTRACSLS DSTTWYCAGL RSRLCSGLSR LRDSWAKALD 60 SARDGSGSHS CPCWRQSRSS GSTWAGLTVQ GSWAPGGHTL SSCPACGTGS SANCSMSMSG120 DPSEPRSRKA ALLPGNVCFS GSSVSFIRGW PPTATSL 157

- (2) INFORMATION ON SEQ ID NO. 460:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 93 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

PPLFPHLLFL WGKVSDSCCF QSAPLRVSGG LPRTQTVHQG LQPLGQHHLV LCRAPQPPVL60 RAESAQGQLG QGSRLCQGWE RLTQLSLLEA EPQ 93

- (2) INFORMATION ON SEQ ID NO. 461:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 328 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

FSLILCKHSI GDRKNYASAK LSELLPEEVE AEVKAAAEIS MGTEVSEEDI CNILHLCTQV 60
IEISEYRTQL YEYLQNRMMA IAPNVTVMVG ELVGARLIAH AGSLLNLAKH AASTVQILGA120
EKALFRALKS RRDTPKYGLI YHASLVGQTS PKHKGKISRM LAAKTVLAIR YDAFGEDSSS180
AMGVENRAKL EARLRTLEDR GIRKISGTGK ALAKTEKYEH KSEVKTYDPS GDSTLPTCSK240
KRKIEQVDKE DEITEKKAKK AKIKVKVEEE EEEKVAEEEE TSVKKKKKRG KKKHIKEEPL300
SEEEPCTSTA IASPEKKKKK KKKRENED

- (2) INFORMATION ON SEQ ID NO. 462:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

YNRNSFLLIL VLSLFFLFLL FLWTSNCCAG TWFFLRKWFF LNVFLFTPFL LLLHRCFFFF 60 CHFFFFLFFN FNFNLGFFGF LFSNFILFIY LFYFAFFRTG WKCGVTRRIV SLHFTFVFIF120 FCFC 124

- (2) INFORMATION ON SEQ ID NO. 463:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

SSFSLFFFFF FFFSGLAIAV LVHGSSSESG SSLMCFFLPL FFFFFTDVSS SSATFSSSSS 60 STLTLILAFL AFFSVISSSL STCSILRFLE QVGSVESPEG S 101

- (2) INFORMATION ON SEQ ID NO. 464:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 427 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

GGSSRRHGGG YAAVALLVLL LLGPGGWCLA EPPRDSLREE LVITPLPSGD VAATFQFRTR 60 WDSELQREGV SHYRLFPKAL GQLISKYSLR ELHLSFTQGF WRTRYWGPPF LQAPSGAELW120 VWFQDTVTDV DKSWKELSNV LSGIFCASLN FIDSTNTVTP TASFKPLGLA NDTDHYFLRY180 AVLPREVVCT ENLTPWKKLL PCSSKAGLSV LLKADRLFHT SYHSQAVHIR PVCRNARCTS240 ISWELRQTLS VVFDAFITGQ GKKDWSLFRM FSRTLTEPCP LASESRVYVD ITTYNQDNET300 LEVHPPPTTT YQDVILGTRK TYAIYDLLDT AMINNSRNLN IQLKWKRPPE NEAPPVPFLH360 AQRYVSGYGL QKGELSTLLY NTHPYRAFPV LLLDTVPWYL RLLHPLPACP GPAATPPPGD420 ADSAAGO

- (2) INFORMATION ON SEQ ID NO. 465:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 128 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

SPSILYGSCT CHSHKAFGGP DTGGHPSCRP HQVQSCGSGS KTLSLMWINL GRSSVMSSQG 60 SSAPLSTSST PPTQSLPLPP SNPWVWPMTL TTTFCAMLCC RGRWSAPKTS PPGRSSCPVV120 PRQASLCC 128

- (2) INFORMATION ON SEQ ID NO. 466:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF .
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

PQAWRRLCRC CSARPVAPGA RRLVPCRTPT RQPAGGTCHH PAAFRGRSRH IPVPHALGFG 60 ASAGRSVPLQ ALSQSPGAAD LQVFSTGAAP VIHTRLLEDP ILGATLPAGP IRCRAVGLVP120 RHCH

- (2) INFORMATION ON SEQ ID NO. 467:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

FLHKTHNRAV EEAKEPFLCL CSRTERGPLA SVSLLVLPGL YQALRRGMET PHSGAWLGEG 60
EAAGVLWASR GYNLSSLGNV CPFVGSSPTR RGTQLYTGTI CVWSVL 106

- (2) INFORMATION ON SEQ ID NO. 468:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 164 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

ISTKQTTHRL SQCKVESPDV SDYCLQMDTR SPESSDYTLE KPKEPLPPPL PQARPQSGAF 60 PYPASRPGTV REEPAGSRWP EGLSQSYYRG IKRAPLLPPQ PCCESCAGIN LRNSPEAETG120 LMPWERSECE PMAPSLLGTN LPKYVKAEGD RDLAEGRKSF SSRN 164

- (2) INFORMATION ON SEQ ID NO. 469:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 108 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

EIRGRPPLFM PPLSCVDEFL QNRPHTDCPS VKLSPPTCRT TAYKWTHVPQ RAQIIPSRSP 60 KNPCRLPFPK PGPRVGRFHT PPQGLVQSGK NQQAHAGQRA SLSPTTEA 108

- (2) INFORMATION ON SEQ ID NO. 470:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 317 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

NMVDYYEVLG VQRHASPEDI KKAYRKLALK WHPDKNPENK EEAERKFKQV AEAYEVLSDA 60 KKRDIYDKYG KEGLNGGGGG GSHFDSPFEF GFTFRNPDDV FREFFGGRDP FSFDFFEDPF120 EDFFGNRGP RGSRSRGTGS FFSAFSGFPS FGSGFSSFDT GFTSFGSLGH GGLTSFSSTS180 FGGSGMGNFK SISTSTKMVN GRKITTKRIV ENGQERVEVE EDGQLKSLTI NGVADDDALA240 EERMRRGQNA LPAQPAGLRP PKPPRASLL RHAPHCLSEE EGEQDRPGAP GPWDPLGVRS300 RIERRWQEEE AEAERGV

- (2) INFORMATION ON SEQ ID NO. 471:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

SMPLVQLPSS FKLLSLLLL PLATFFQSCC GRRGGPRARV PQVGPARPPP QRDSEARVSA 60 ARQAGAASAG GGRQAGLAGR SGLSACAPQR GHRRRPHHLL LRTLTGHLLQ LLLFLDRSRQ120 FSL

- (2) INFORMATION ON SEQ ID NO. 472:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 105 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

- (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

KIRSNQCLWS NFLPPSNSSL CFCFFLLPPS FNPAADAEGV PGPGCPRSVL LALLLRETVR 60 RVSQQRGRPG RLRRAEAGRL GWQGVLASPH ALLSEGIVVG HTIYC 105

- (2) INFORMATION ON SEQ ID NO. 473:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 159 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

IVSERSLRSL WTAHWALPEM DSRIPYDDYP VVFLPAYENP PAWIPPHERV HHPDYNNELT 60 QFLPRTITLK KPPGAQLGFN IRGGKASQLG IFISKVIPDS DAHRAGLQEG DQVLAVNDVD120 FQDIEHSKAV EILKTAREIS MRVRFFPYNY HRQKERTVH

- (2) INFORMATION ON SEQ ID NO. 474:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

- (2) INFORMATION ON SEQ ID NO. 475:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

LGGLSSSDVK SQLSSRRLLQ CDGSGQKLGQ LIVVVRVVYP LMRRNPCWRI LIGRQENHRV60 VIIRNPAVHL GQGPVGSPQR PQTPLTDNSV WEPEADA 97

- (2) INFORMATION ON SEQ ID NO. 476:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 274 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

GHLWRPAGGR LPRHHDQVCR AAEPHRGGGL CGHQRRLPHR PRVQEGWGLC PHESLHQVPA 60 DRPWHEPGAG CAADCEDPHR RPGACEPGAP PAARAAGLGR GTRHGNGDIL SFEDANRAMQ120 TGVTGIMIAR GALLKPWLFT EIKEQRHWDI SSSERLDILR DFTNYGLEHW GSDTQGVEKT180 RRFLLEWLSF LCRYDPVGLL ERLPQRINER PPYYLGRDYL ETLMASQKAA DWIRISEMLL240 GPVPPTSPSC RSTRPTRTSS LRLSQGHPGA RRVQ

- (2) INFORMATION ON SEQ ID NO. 477:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 256 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

AGPAPVQPGP HTRCRCPRGH GSRGRSQAGK LWCPAGPRRP GTSTPPSSPV RTCGPLTDED 60 VVRLRPCEKK RLDIRGKLYL APLTTCGNLP FRRICKRFGA DVTCGEMAVC TNLLQGQMSE120 WALLKRHQCE DIFGVQLEGA FPDTMTKCAE LLSRTVEVDF VDINVGCPID LVYKKGGGCA180 LMNRSTKFQQ IVRGMNQVLD VPLTVKIRTG VQERVNLAHR LLPELRDWGV ALVTEMGTSC240 HLRMPTAPCR LVSPGS 256

- (2) INFORMATION ON SEQ ID NO. 478:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 165 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

NLLYSPRPRV PLGKPEATCT RWPCASARRR GGGHWPKEHL ADADPVGCLL AGHQRLQVVA 60 AQVVGRPLVD PLWEPLQQPH GIVPAQEGQP LEQKAPGLLH ALRVRAPVLQ AVVGEVPQDV120 QALGRRDVPV PLLLDLREEP RLEQGATGNH DPGDTSLHGA VGILK 165

- (2) INFORMATION ON SEQ ID NO. 479:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 262 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

- (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

GSPMSPARAM QTLFVPEHGD HGAGVCSDHH HRGGHVPAEP LQAVCTVLHQ PAQPGAEERR 60 CPVLRRMPVA SETQCQATES QSRSLTPRLG PPTAWPCALR PAERFPPLPA QCLLHVQLQT120 LFVPEHGDHG AGVCSDHHHR GGHVPAEPLQ AVCTVLHQPA QPGAEERRCP VLRRMPVALG180 EHSVRQRNPR AAGLRPASAH RPPGRAALRP AGALPPLPAH LSVPAARDRP AAHHLAVRRG240 GAPTLPGPLD LQGSGPRGGV GN

- (2) INFORMATION ON SEQ ID NO. 480:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 270 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

AAQCLLHVQC KRSLFQSMEI TELEFVQIII IVVVTCLLSH YKLSARSFIS RHSQGRRRED 60
ALSSEGCLWP RRHSVRQRNP RAAVLRPASA HRPPGRAPFA QRSVFHRCQP NVSCTCNCKR120
SLFQSMEITE LEFVQIIIIV VVTCLLSHYK LSARSFISRH SQGRRREDAL SSEGCLWPSE180
STVSGNGIPE PQVYAPPRPT DRLAVPPFAQ RERFHRFQPT YPYLQHEIDL PPTISLSDGE240
EPPPYQGPWT FKVRDPEEEL EIERGLGAET 270

- (2) INFORMATION ON SEQ ID NO. 481:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 124 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

ATTSCLHGPS SAGTARGGGE KMPCPQKDAC GPRRAQCQAT ESQSRRSTPR LGPPTAWPCR 60 PSPSGSASTA SSPPIRTCST RSTCRPPSRC QTGRSPHPTR APGPSRFGTP RRSWKLNGDW120 VRRP

- (2) INFORMATION ON SEQ ID NO. 482:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

RVLVSPLSLS MWRWKVEKDT VSILKLLRFS ERGRHLNRQV GFSVLSALGI WREMGLLSLC60 TQEGHALKTV FVDQRRLYST GGIQMSLRGR EETWQADYI 99

- (2) INFORMATION ON SEQ ID NO. 483:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 104 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

VLEEEKKHGK QITSEPFELC FSFFPCLFSK IYLNLETQDI FLGNLLPMSE VASAASRQIP 60 GNPEPQNVIP PGSAWPDPVL SAGFTYQSHS SFSINTPKSS PNHH 104

- (2) INFORMATION ON SEQ ID NO. 484:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

KLDSTQCRPS LHTNMYVLLS ECHLLCTQCH DSKIKISVSN QNINQARNSW AQRGVRGLSY 60 TAVKQPTCSA HSQAESDWSC RQRGGGRVLC CPLLCMVSWV FQGGQLLSPN KTVNSLRTGP120 LPH

- (2) INFORMATION ON SEQ ID NO. 485:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 303 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

LGRKPSWVGG AGLEPSQGSG LSHHPAPQSD SAPTSPPIPG EPGPQREVDK WGGSLGRPES 60
SGHPGRTPAT CCHCAAVMAR SGSATPPARA PGAPPRSPPQ RLVQDVSGPL RELRPRLCHL120
RKGPQGYGFN LHSDKSRPGQ YIRSVDPGSP AARSGLRAQD RLIEVNGQNV EGLRHAEVVA180
SIKAREDEAR LLVVDPETDE HFKRLRVTPT EEHVEGPLPS PVTNGTSPAQ LNGGSACSSR240
SDLPGSDKDT EDGSAWKQDP FQESGLHLSP TAAEAKEKAR AMRVNKRAPQ MDWNRKREIF300
SNF

- (2) INFORMATION ON SEQ ID NO. 486:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 149 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

APRRPRPRR LEPCESTSAR HRWTGTGSVK SSATSEPLPA CLGTLGPLPH GPWASACPEL 60 PQPQWTGGWS CHCPEISPSP GEPPSCPCPP GTGGLWQQDR GRETQRCERE SETETERERE120 RHRERQRESE RARGSRGARA FAALPGPAD 149

- (2) INFORMATION ON SEQ ID NO. 487:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 217 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

FLGNGRTTLQ STEAGGARGR LRPKVRAGGV PGSRDRQEGA QKLLKISRFL FQSICGARLL 60 TRMARAFSLA SAAVGLRWRP LSWKGSCFQA LPSSVSLSEP GRSLRDEHAE PPLSWAGLVP120 LVTGDGRGPS TCSSVGVTRS RLKCSSVSGS TTSSRASSSR ALMLATTSAW RSPSTFCPFT180 SMSRSWARRP ERAAGEPGST ERMYWPGRDL SLCRLNP 217

- (2) INFORMATION ON SEQ ID NO. 488:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 298 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

EIRAVGGGVC VDGMGTPGEG LGRCSHALIR GVPESLASGE GAGAGLPALD LAKAQREHGV 60 LGGKLRQRLG LQLLELPPEE SLPLGPLLGD TAVIQGDTAL ITRPWSPARR PEVDGVRKAL120 QDLGLRIVEI GDENATLDGT DVLFTGREFF VGLSKWTNHR GAEIVADTFR DFAVSTVPVS180 GPSHLRGLCG MGGPRTVVAG SSDAAQKAVR AMAVLTDHPY ASLTLPDDAA ADCLFLRPGL240 PGVPPFLLHR GGGDLPNSQE ALQKLSDVTL VPVSCSELEK AGAGLSSLCL VLSTRPHS 298

- (2) INFORMATION ON SEQ ID NO. 489:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 175 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

AGHRYQGDIR ELLQCLLAVG QIPTSTVQEE RGHTRQPRTK KETVSSCVIW EGQGGIWVIC 60 QHCHCPDSLL GSVAAACHNS ARSPHAAETA QVGGTRDWHS GDGEVPERVR HDLSSSVIGP120 FGEAYEKLPA GEENVSAIQR RVLVSYFHNS EPQVLQGFAD SIDLWPTSGA PGPRD

- (2) INFORMATION ON SEQ ID NO. 490:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 150 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

LGPCPLGSRP CRQAAVPAAM TPQVAVLAAV APVVASVYLP APRAPFELWP DPEREGQPPH 60 LPPTPGSLGL PGSGHGSSGP APPPASPSHP HRLPLQPLGF LSFLVSSPVS SGHPHSCRAV120 ISAGAPPPED RVGGEGSPRL QASGTGSSGF.

- (2) INFORMATION ON SEQ ID NO. 491:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 89 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

FVKRTKQPRQ TLDAPCSALR LWGRCLLGEA VAQGVHCEAG PVDSAGGIHL ASGCLVSVYS60 DIAFCCHLSC GQRGVSWHEN IFFFKCGSF 89

- (2) INFORMATION ON SEQ ID NO. 492:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 63 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

LTHLLFEKCL LPSLGLITKF DHDHIVVSQS ALEIVSGLHE VAMGVWSTLK LYQSCTYFQT60 FLK 63

- (2) INFORMATION ON SEQ ID NO. 493:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 73 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

DGSRMLCHYI QKQDNLKLNG CPLQSQQVQP HSARPELQPL PKGIFPTAST PSKEHQGFVS60 VVLFFLQTID IYS

- (2) INFORMATION ON SEQ ID NO. 494:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 318 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

KCATFWSFPR RQGGLGIAIS EEDTLSGVII KSLTEHGVAA TDGRLKVGDQ ILAVDDEIVV 60 GYPIEKFISL LKTAKMTVKL TIHAENPDSQ AVPSAAGAAS GEKKNSSQSL MVPQSGSPEP120 ESIRNTSRSS TPAIFASDPA TCPIIPGCET TIEISKGRTG LGLSIVGGSD TLLGAIIHE180 VYEEGAACKD GRLWAGDQIL EVNGIDLRKA THDEAINVLR QTPQRVRLTL YRDEAPYKEE240 EVCDTLTIEL QKKPGKGLGL SIVGKRNDTG VFVSDIVKGG IADADGRLMQ GDQILMVNGE300 DVRNATQEAV AVWIKVFP

- (2) INFORMATION ON SEQ ID NO. 495:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 206 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

SAFAEMGSDH TQSSASKISQ DVDKEDEFGY SWKNIRERYG TLTGELHMIE LEKGHSGLGL 60 SLAGNKDRSR MSVFIVGIDP NGAAGKDGRL QIADELLEIN GQILYGRSHQ NASSIIKCAP120 SKVKIIFIRN KDAVNQMAVC PGNAVEPLPS NSENLQNKET EPTVTTSDAA VDLSSFKNVQ180 HSGASQGGRG VWVLLSAKKI HSVESS

- (2) INFORMATION ON SEQ ID NO. 496:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 119 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

TSWIIMAPSS VSEPPTMLRP SPVRPLEISM VVSQPGIMGQ VAGSEAKIAG VDDLLVFRMD 60 SGSGEPDCGT IRDWELFFFS PLAAPAAEGT AWESGFSAWM VSFTVIFAVF RRLINFSIG 119

- (2) INFORMATION ON SEQ ID NO. 497:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

SAPSLTKCRS THVYPLSLIM FMSGGSSRST LRRMVPTPST TSLSPRSSSS TSKLLTQSGP60 SLPQPPASRP F

- (2) INFORMATION ON SEQ ID NO. 498:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 139 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

SRSPACGASE HGDGAMSLIC SISNEVPEHP CVSPVSNHVY ERRLIEKYIA ENGTDPINNQ 60 PLSEEQLIDI KVAHPIRPKP PSATSIPAIL KALQDEWDAV MLHSFTLRQS CRQPAKSCHT120 LCTSTMPPAV SLPVSPRKL

- (2) INFORMATION ON SEQ ID NO. 499:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 74 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
     (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

TTGRERGCRP CAGLFYCFLF LMKLDHCLQN PAQALLPIPF TVSLVRRAMT RQAASCWYRA60

CDSSWRVVCS SGAE

74

- (2) INFORMATION ON SEQ ID NO. 500:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

FSFFNETRSL LTKPCTSPPA HPLHSSLGSA SPVSQELQQN GCGTATTTSI ERQEGRGAVG60 LVQGFFIVFF F

- (2) INFORMATION ON SEQ ID NO. 501:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 284 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

EARGLATRTR SGAAAHAGDR FTDADDVAIL TYVKENARSP SSVTGNALWK AMEKSSLTQH 60 SWQSLKDRYL KHLRGQEHKY LLGDAPVSPS SQKLKRKAEE DPEAADSGEP QNKRTPDLPE120 EEYVKEEIQE NEEAVKKMLV EATREFEEVV VDESPPDFEI HITMCDDDPP TPEEDSETQP180 DEEEEEEEEK VSQPEVGAAI KIIRQLMEKF NLDLSTVTQA FLKNSGELEA TSAFLASGQR240 ADGYPIWSRQ DDIDLQKDDE DTREALVKKF GAQNVARRIE FRKK 284

- (2) INFORMATION ON SEQ ID NO. 502:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 123 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

ETFSSSSSS SSGCVSESSS GVGGSSSHIV ICISKSGGLS STTTSSNSRV ASTSIFLTAS 60 SFSWISSFTY SSSGKSGVLL FCGSPLSAAS GSSSAFRLSF WEEGLTGASP SRYLCSWPRR120 CLR

- (2) INFORMATION ON SEQ ID NO. 503:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 175 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

VFLRCGWIII THSYMYFKIR RALIHHNLLK LPGGFHKHLF DCFFILLDFF LHILFFRQIW 60 SSLILWFPAI RGLRVLLRLP LELLGGGAHR RVPQQVLMLL APQVLEVAVL QGLPRVLRER120 ALLHRFPQGV TGDGAGRAGI FLHVGKDGYV VRIREAIARV RCRSAPRARR QAPGF 175

- (2) INFORMATION ON SEQ ID NO. 504:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 78 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

CPPEKSLQMF QPLSSPDSHR KGTGFGLGIV FSLTFFKRRM WPLAFGSGMG LGMAYSNCQH60 DFQAPYLLHG KYVKEQEQ 78

- (2) INFORMATION ON SEQ ID NO. 505:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 95 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

SKTSTLPVAI WTRQRLEHLQ GFLGWTSITR ILSSRPHPPD TGPTSCRAPT QTCSPPAPPA60 FLSAGPRAPT PESLARAGNK SQVRKAGADA PDIAR 95

- (2) INFORMATION ON SEQ ID NO. 506:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 156 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

AIPNPMPEPK ANGHILLKK VSEKTIPNPK PVPFLWLSGL DRGWNICRDF SGGHQLPGFY 60 LHDRIRQTPV PLPAELRLRH VPHPRLQLSS RPAPALRPLK VSRELETSPR SGRQAQTLQI120 SRDDPLLPSL PVFSVGRQGD AVVWRLEVTL TLGCAY

- (2) INFORMATION ON SEQ ID NO. 507:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 169 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEOUENCE DESCRIPTION: SEO ID NO: 507:

AASGMLGSWP ARTFHPGACV SRRPSAPWKH TASGKDSPDL RFSEHGVSQE FWAGGLVAVL 60 EMTPSPSPWG TQEGPAGMCS LWVVGWCPCR GAGVRDLVLV HAGVWCKHVC AVQRDACGES120 RTPAPPRKGG AVTSVLCLFL IKTFPLFSYK FASCKQVHKD PPLVKSGFE 169

- (2) INFORMATION ON SEQ ID NO. 508:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 155 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

TQNTGNRSAF PGWRWCAALS TRVSLYSTYM FTPHTCVDEH QITHPSSTTG TPADYPQAAH 60 SGRALLGAPR GGARGHLQHC HQAASPEFLG NTVLGKPKVR AVLPRGRVLP GCGGPAADTG120 PRVEGPGRPA SKHARRSLGE PGSVASSLLS LRSPI

- (2) INFORMATION ON SEQ ID NO. 509:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 148 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

ENRGNVLIKN KHKTLVTAPP FLGGAGVRLS PHASLCTAHT CLHHTPAWTS TRSRTPAPRQ 60 GHQPTTHRLH IPAGPSWVPH GEGLGVISST ATRPPAQNSW ETPCSENRRS GLSFPEAVCF120 QGAEGRRLTQ APGWKVLAGQ LPSMPDAA 148

- (2) INFORMATION ON SEQ ID NO. 510:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

NAYISGYERD FMTIQSNITL ADRETEVFHD LPSLPASLRQ NWIPTLVFFL PFTSFSLLYN60 VLRDQNSHQN RLFLR 75

- (2) INFORMATION ON SEQ ID NO. 511:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 67 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

FRDTEGLLAL MTFWMGLQLM TILILEERTL LIFSPIALLR RSTSYSESLH IPLVFLQAPE60 PLVQMLY 67

- (2) INFORMATION ON SEQ ID NO. 512:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

IFFFFFFFF PLRHLFNNCR NPKELASNLE VVSEAAGWLD WAQPLSCLNR PRNGIMMTMR 60 TSILSSSHCV YYVFSFNKAF VPMALELGGR LKECVVILSK M 101

- (2) INFORMATION ON SEQ ID NO. 513:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 179 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

FGTMGGISDP DTLHIWKTNS LPLRFWVNIL KNPQFVFDID KTDHIDACLS VIAQAFIDAC 60 SISDLQLGKD SPTNKLLYAK EIPEYRKIVQ RYYKQIQDMT PLSEQEMNAH LAEESRKYQN120

EFNTNVAMAE IYKYAKRYRP QIMAALEANP TARRTQLQHK FEQVVALMED NIYECYSEA 179

- (2) INFORMATION ON SEQ ID NO. 514:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 179 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

DRGAPALTPG HLHPLPPVPR SVSGMEAREL VRLPHLPSTA CTVPTHLLHN VQLVLLPRAP 60 CIQAAKHKLG ERRPPARRLQ PRNSTSSTLV QGALLELTFD WFLLQLPKCY LHFPLTRRGS120 WPQTVSSSVR FLLLGRLLVE WAVPAPWGAL WASPGAGRVE GRDGGHRSWE PRLQEKERG 179

- (2) INFORMATION ON SEQ ID NO. 515:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 200 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

SGDRWEGMEV PRGQGGGAPV SESSPSSCPR PSRLCSVFPS LSHRHGVEDQ VEAQWASISP 60
SSSLTNSPCV SGLTVALVDV VLHQSHHLLK LVLQLCPPGR GVGLQRGHDL RPIPLGVLIN120
LCHGHIGVEL ILVFPRLLGQ MGIHLLLAER RHVLDLLVVA LHDLPVLRNL LGVEELVGWR180
ILAQLQVRDG AGVDEGLRDD 200

- (2) INFORMATION ON SEQ ID NO. 516:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 157 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

TSMEALLFRL FKLPATTLRC IGLRRPLVTH TLRRKCEHKA SRLCHGGCCC TLEPCVGRHR 60
DWDLERGKSS AKTGGELHGR RTAAARGGSE RPVLGHRRRD PDAGGLRGQD GEALQHRGWH120
IPGSETLPGR GGHVPWPRPG RRHPHHMCGF WDSQSLA 157

- (2) INFORMATION ON SEQ ID NO. 517:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 401 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

RTRCAGSVNT KPPGFVMAAA AARWNHVWVG TETGILKGVN LQRKQAANFT AGGQPRREEA 60
VSALCWGTGG ETQMLVGCAD RTVKHFSTED GIFQGQRHCP GGEGMFRGLA QADGTLITCV120
DSGILRVWHD KDKDTSSDPL LELRVGPGVC RMRQDPAHPH VVATGGKENA LKIWDLQGSE180
EPVFRAKNVR NDWLDLRVPI WDQDIQFLPG SQKLVTCTGY HQVRVYDPAS PQRRPVLETT240
YGEYPLTAMT LTPGGNSVIV GNTHGQLAEI DLRQGRLLGC LKGLAGSVRG LQCHPSKPLL300
ASCGLDRVLR IHRIQNPRGL EHKVYLKSQL NCLLLSGRDN WEDEPQEPQE PNKVPLEDTE360
TDELWASLEA AAKRKLSGLE QPQGALQTRR RKKKRPGSTS P

- (2) INFORMATION ON SEQ ID NO. 518:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 222 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

SWEKLYVLVP DGNPQVQPVI PHVLGPEHRF LRALQVPYLQ SILFPTCGNH MGVCWVLAHP 60 THPRAHSQFQ EWVRGCVLVL VMPDSENPRI HTCDEGAVGL GEATEHALPA RAVSLTLEYA120 ILGAEVLHRP VRAAHQHLGL AAGAPTQGAH CLLAPRLSSG REVRRLFSLK IYPFQDPSLG180 ADPHMVPACS SSRHDKAWRL CVHTSGAACA SPAGVEVRCT AV 222

- (2) INFORMATION ON SEQ ID NO. 519:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

DPRPVSLLTL ALLPRCHFLS SSVKYRLHIL SLNASTICVT PKDFWDFDET CEGEDTEKPV60 ICKHLLLFPH HLWDISAVVS KWQIIN 86

- (2) INFORMATION ON SEQ ID NO. 520:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 77 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

ISSVNYHMTI QAQYKLGHCI LCGWISVAVF LTSPKKTSCR AELLVQAPDN DAPDFAFWGL60 SLLLSHFLKL FAWPWHH 77

- (2) INFORMATION ON SEQ ID NO. 521:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

CGNKSKCLQI TGFSVSSPSQ VSSKSQKSLG VTQIVLALSD KMCSLYLTEE ERKWHLGSSA60 RVSKETGLGS Q 71

- (2) INFORMATION ON SEQ ID NO. 528:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 120 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

LTYLTTTTT FTLGRSLGFI REVGTLTRSE APPSHGVGDS GGRGNPSEHP GGGWSMYFR SC LPHLFHGVPC QGQALICGEG SKQRRRPFRG GERAVAPRTP SPAHDIPEKE TKIKPRGLST120

- (2) INFORMATION ON SEQ ID NO. 529:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 90 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

PLLKGKKLSA ALTNLSFFFF FFFFFGKKPW LYSLCGDTVP FRGPSQPWGG GQWWAWESQR60 ASWRVRRLHV FCSSPSFPWG PLPGSSTNMW 90

- (2) INFORMATION ON SEQ ID NO. 530:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

NKAPGPFYVG APLKYGMVVG REAVAQQSLS PDYQLWGGFQ GARSRLGSSS HRHVGGGRKY60 LQGGTVSEEQ DGRGFSACYG ILFKEMGVKP GTVAHA 96

## (2) INFORMATION ON SEQ ID NO. 531:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 497 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

TPALVQRFRE GGSGAPEQAE CVELLALGE PAEELCEEFL AHARGRLEKE LRNLEAELGP 60
SPPAPDVLEF TDHGGSGFVG GLCQVAAAYQ ELFAAQGPAG AEKLAAFARQ LGSRYFALVE120
RRLAQEQGGG DNSLLVRALD RFHRRLRAPG ALLAAAGLAD AATEIVERVA RERLGHHLQG180
LRAAFLGCLT DVRQALAAPR VAGKEGPGLA ELLANVASSI LSHIKASLAA VHLFTAKEVS240
FSNKPYFRGE FCSQGVREGL IVGFVHSMCQ TAQSFCDSPG EKGGATPPAL LLLLSRLCLD300
YETATISYIL TLTDEQFLVQ DQFPVTPVST LCAEARETAR RLLTHYVKVQ GLVISQMLRK360
SVETRDWLST LEPRNVRAVM KRVVEDTTAI DVQVGLLYEE GVRKAQSSDS SKRTFSVYSS420
SRQQGRYAPS YTPSAPMDTN LLSNIQKLFS ERIDVFSPVE FNKVSVLTGI IKISLKTLAG480
SVCGLRTFLA LCGLQQG

## (2) INFORMATION ON SEQ ID NO. 532:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

CGSGWSWPHW PATRPGQGPP SQPREVLPAP GGRLSGSPGR PPGDPAGGGP GARGPLVPRS 60 PWQRLRARQR PAGPREPASA GGSGPAPAPA VSCHHHPAPA PAAAPPAQNS GCPAAGRRPP120 ASRHLLGPGP QTAPGRPPPP GRGRPRSHCL HGR

(2)	INFORMATION	ON	SEQ	ΙD	NO.	533:
-----	-------------	----	-----	----	-----	------

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 221 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

YDQALHLHVV GQQPPRRFPG LCTQRAHGRH WELILHQKLF ISESEDVGDG GRLVVQAEAG 60 EQQEQGRWCG TPLLPRAVAE ALSRLAHRVD EAHDEALTDT LTAELTPEVG LVGEGHLFGG120 EKVHCCQRGL NVAQDGAGHI GQQLGQARAL LPSHARCCQR LADVCQAAQE GRPETLQVVA180 QALAGHSFHD LRGSVCEPGS GQQGPGSPQA PVEAVQRPHQ Q 221

- (2) INFORMATION ON SEQ ID NO. 534:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 52 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

PSILIPMTPG GFFSVMVRAK TGSTHRCSPA VYPLMRRIPC WRILIGRQET TG

.52

- (2) INFORMATION ON SEQ ID NO. 535:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 38 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

MOLECULE TYPE: ORF (ii) (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535: AGKKPPASHH KESGCPSRPS PTGHSTPPSD PLTDNSVW 38 (2) INFORMATION ON SEQ ID NO. 536: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 55 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ORF (iii) HYPOTHETICAL: yes ORIGIN (vi) (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536: SGCVPSHEED SMLEDSHRQA RNHRLVIIRN PVVHLGQAPL ATPHRPQIRS LTIQS (2) INFORMATION ON SEQ ID NO. 537: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 113 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear MOLECULE TYPE: ORF (ii) (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537: TRGPRKRLRR SGRRGGLRSW AGRERVLGTA LLGIYIVFPR IPGSGSEEAV TPYDRRDLDS 60

RNSPQAPAGQ STTSSSFCFC DGLESRGLKH TVSIDCIRFV QKPGQLTESH FLA

- (2) INFORMATION ON SEQ ID NO. 538:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

EPADSQARGR QCLLLLHQVQ GIWLKACIFP GHKLPEPLKW EARQFQTNLF STHHSTFKVC 60 LLLLPVHPPS LQFFHSLTSE RVPGGSMVNK LTCMLQKKKK K 101

- (2) INFORMATION ON SEQ ID NO. 539:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 198 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

YSLCSQCVSA PLTLNRHRSR RKRKWWIAQL EPGDCYDCLD LCGHRASQPP QTLSLECGGT 60 QCRFPGGLSP RPSPCPPSSS GLLFYRFFLV SFLGLLFTEG TAALGFLVTS ALLGSDGSAS120 ASWDLGMGTM MASTQMSWKM APRKSPYRSR FSRKVGSGTS GGEKSRSEAM AQVACCLTSL180 LTHHSLEPTP APPRRSPR

- (2) INFORMATION ON SEQ ID NO. 540:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 147 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

KKNSSALIFL EEAADFGCQI SLRNGHFLRC FFLTESVDKL IKRLSHFKIT PKSSSTVFFF 60 FSFCFKITNQ VRSPTSSSMN SFVTELLSVC SPHCALNTVS AAPVCPLFRK ESIFNTFTIC120 TPWNLHMLTS YYKPTHPQLS SGTGHPL

- (2) INFORMATION ON SEQ ID NO. 541:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 138 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

KNDRFPWTSL PGLKGALIKL FTEHVAEKHI YGLMPLLLEA QSTPFQVTPS TMANIVKGLY 60 TLRPEWVQMA PTLFSKFIPN ILPPAVESEL SEYAAQDQKF QRELIQNGFT RGDQSRKRAG120 DELAYNSSSA CASSRGYR 138

- (2) INFORMATION ON SEQ ID NO. 542:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 179 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

KACIPSDQSG FRWLQLYFLN LFQTFSLRRW NLNFLNMLLK IRNFKENLYR MVLQGVTSPG 60 RELGMSWLII ARQHVQVPGG TDSECIEYAF LPEKRTHWSC RDCIQSTVGA AHTQELCHKA120 VHGRGCWTSI LVCNFKTKTK KKKNSAARLG GDFZMGQSFW ZFIIRFCZZK ASQKVTISK 179

- (2) INFORMATION ON SEQ ID NO. 543:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 92 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

IQFLEAAFAV FLHCMRFGNE CRNLLWAFTF LCQFGFYCLN LMLTWRGDGG QCCCGASSES60 VCGELCCADV AVGGQVRGSA PSWKKSCLRV YV 92

- (2) INFORMATION ON SEQ ID NO. 544:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 99 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

KPNWHRKVNA HSKFLHSFPN RIQCKKTAKA ASRNCIYWPL PEQQAAMPAP WPPELDACCA60 DVLTLMRMLG YGSDSEEIHL SYSSLERSSC VFNMKHFIW 99

- (2) INFORMATION ON SEQ ID NO. 545:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

QSQNTKVFVP IRIYTDPLTK VLLIMQFASS PSSWLGSSPI WHDHIKRTPS DMISSKKVPS60 LLPDHQRPHQ HNTTLRIQIH CWPHNSTVPH LLSRSA 96

- (2) INFORMATION ON SEQ ID NO. 546:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 108 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

GRDAGQSEPW LSTSGCCAWG GCAPGARGCW GPGPPSLGVG RKPGCRVSAS SVPERWIAWS 60 PRPSEASATF RGAPKSILTA RLWASAWRPQ HRGSQNERPW SSSMKTSG 108

- (2) INFORMATION ON SEQ ID NO. 547:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

PGRRAKRAMA VYVGMLRLGR LCAGSSGVLG ARAALSRSWQ EARLQGVRFL SSREVDRMVS 60 TPIGGLSYVQ GCTKKHLNSK TVGQCLETTA QRVPEREALV VLHEDVRLTF AQLKEEW 117

- (2) INFORMATION ON SEQ ID NO. 548:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

PLLLELGKGQ PDVFMEDDQG LSFWDPLCCG LQALAHSLAV KMLFGAPLNV AEASDGRGDH 60 AIHLSGTEEA DTLQPGFLPT PREGGPGPQH PRAPGAQPPQ AQHPDVDSHG SLCPASR 117

- (2) INFORMATION ON SEQ ID NO. 549:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 68 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

RLSGPAANPR GAAGWRAAGA QELGMSYKPM RPWLPSSTPW SARHPLGPGA PRFPDREACA60 CAVRGCSV

- (2) INFORMATION ON SEQ ID NO. 550:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 68 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

GHCSPARRTR TPPCQGTGVP RAPGGAWQTR GCCWAARGAW VCRTSPTPGR QRHASRPLLG60 GWLRGRSA

- (2) INFORMATION ON SEQ ID NO. 551:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 68 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

DTAAPHGARA RLPVREPGCP GPQGVPGRPG GAAGQPGAHG FVGHPQLLGA SGTPAGRSSG60 VGCGAAQP

- (2) INFORMATION ON SEQ ID NO. 552:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 32 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

(111) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:	
SPISITETQQ FSNNLIHTIT CLLRMALYLF SL	32
(2) INFORMATION ON SEQ ID NO. 553:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 33 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:	
ITLQPISQNM FLLLNNTQLF YLCVLFMPDH QYQ	33
(2) INFORMATION ON SEQ ID NO. 554:	,
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 43 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:	

- (2) INFORMATION ON SEQ ID NO. 555:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 85 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

CFTHWNVFPR LWMTSFLMER VQEGWKTPGF KLSIPHMGFS IIFRPEAARP EVRLHLSALF60 VLLLATLGFL LGTMCGCGMC EQKGG 85

- (2) INFORMATION ON SEQ ID NO. 556:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

FNDGKTWQLK KTLVTNGGFL LFFPHPPFCS HMPQPHMVPS RNPKVARSST KRADKCRRTS 60 GRAASGLKMI EKPMWGMLSL NPGVFHPSWT LSIRKEVIHN RGKTFQ 106

- (2) INFORMATION ON SEQ ID NO. 557:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 109 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes
(Vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:
NINYIEIIFL FLLLISPLGP HRLSPAQLAQ LAQLAHSPQV SRRHRALTMV GWHGVSNVAN 60 SSHHPHPHSP SQRPLVVGPA VFQKGLTCTN LRQTYAPFSV SLASPSWED 109
(2) INFORMATION ON SEQ ID NO. 558:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 50 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:
LGIFVAYRNQ LGVPSLMRCS WKAIYARGGF TFVAPPFIDP SAFKKLECEN 50
(2) INFORMATION ON SEQ ID NO. 559:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 44 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

(vi) ORIGIN
(A) ORGANISM: HUMAN

(2) INFORMATION ON SEQ ID NO. 560:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 45 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:	
RVNEWRSDKS ETTSCINGFP AASHKRRYTK LVPVSYKNAK LRMGV	4.5
(2) INFORMATION ON SEQ ID NO. 561:	·
<ul><li>(i) SEQUENCE CHARACTERISTIC:</li><li>(A) LENGTH: 34 amino acids</li><li>(B) TYPE: Protein</li><li>(C) STRAND: individual</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: ORF	,
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:	
MRSRLPCEGL VARHPRELRV PSVRFWIDWP WVLT	34
(2) INFORMATION ON SEQ ID NO. 562:	
(i) SEQUENCE CHARACTERISTIC:  (A) LENGTH: 67 amino acids  (B) TYPE: Protein  (C) STRAND: individual	

(ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

VSTHGQSIQK RTEGTRSSRG CRATSPSHGN RLLIQESFPQ NPPRARFQGH PLGRQSRQQP60 FTEAMSQ 67

- (2) INFORMATION ON SEQ ID NO. 563:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 50 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN.
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

APMASQSRSA LRARVAHAGA VPPALHTAID SSFRNHFLKT HQGLGSKGTR

50

- (2) INFORMATION ON SEQ ID NO. 564:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 54 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

(2) INFORMATION ON SEQ ID NO. 565: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 57 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ORF (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565: CTMVNVDNTV SFLSSFLNVN LYLTQSVCLK LLRTFPNVTG PFPFVIRGIL FQDYCCV 57 (2) INFORMATION ON SEQ ID NO. 566: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 49 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ORF (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566: EKCQPHSLIL LWPFNFILIK SHRSHTTIIL KQNSSDYKGK WASNVGKCP 49 (2) INFORMATION ON SEQ ID NO. 567: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 94 amino acids (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

  GEGRVWNPEG SKSRHWPDHP APWAPSPRQE QLFSIPSQTS SIFITMTFRE VSQASSRCPT60

  IPSGGKRQEN SPRVPVMLLS PSQFRLSRTS YLQP

  94
- (2) INFORMATION ON SEQ ID NO. 568:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 89 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

GLTLKKGTFP RGPEIQADPN LTPCSRTQAH RPLNSNPTSP PPPPTPDFLI SWNAFQDWKS60 PQGSSEPILS PARISSMHPG HAFHISRNK 89

- (2) INFORMATION ON SEQ ID NO. 569:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 89 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

DVLDSLNWDG ESSMTGTRGE FSCLFPPEGI VGHLELAWET SLKVIVIKIE LVWEGMENSC60 SCLGLGAQGA GWSGQCLDLL PSGFHTRPS 89

- (2) INFORMATION ON SEQ ID NO. 570:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 73 amino acids

    - (B) TYPE: Protein(C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

KSIAHSVIGY FHDFKWFYEE TESSDDVEVL TLKKFKGDLA YRRQEYQVEF NIWCLKWALV60 LSVMAYVNNS VPS

- (2) INFORMATION ON SEQ ID NO. 571:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 40 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

SADSQEIQRR PGLQTTRVSG RIQHMVLEVG SCFISYGICK

40

- (2) INFORMATION ON SEQ ID NO. 572:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 60 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

NKSPLQAPYV EFYLILLSSV GQVSFEFLES QHFNIITAFC FFIKPLEIMK IAYYRVSYAF60

- (2) INFORMATION ON SEQ ID NO. 573:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 318 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

GNLSLESLCN LYNWRYKNLG NLPHVQLLPE FSTANAGLLY DFQLINVEDF QGVGESEPNP 60
YFYQNLGEAE YVVALFMYMC LLGYPADKIS ILTTYNGQKH LIRDIINRRC GNNPLIGRPN120
KVTTVDRFQG QQNDYILLSL VRTRAVGHLR DVRRLVVAMS RARLGLYIFA RVSLFQNCFE180
LTPAFSQLTA RPLHLHIPT EPFPTTRKNG ERPSHEVQII KNMPQMANFV YNMYMHLIQT240
THHYHQTLLQ LPPAMVEEGE EVQNQETELE TEEEAMTVQA DIIPSPTDTS CRQETPAFER300
ESRPGGEGAI ALGGLGCF

- (2) INFORMATION ON SEQ ID NO. 574:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 67 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

KTPKPPQRNC PFPTGAALTL KGWSFLTAAG VCWTGYDVSL NSHGLFFCFO LCFLILNFLT60

- (2) INFORMATION ON SEQ ID NO. 575:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 155 amino acids

    - (B) TYPE: Protein (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - ORIGIN (vi)
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

SLMIMMCSLY QMHVHVVYKV CHLGHIFYYL YFMRWSLSIL SSSWERFCWN YMQMKGASCE 60 LTESWSQFKT VLEEGYSGED IKSKSGSRHG HYQATDIPQM AHCPGSYQRK KNIVILLTLK120 SINSCHLVWS SNQWIVSTSS IDDVANKMLL AIICC

- (2) INFORMATION ON SEQ ID NO. 576:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 57 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - MOLECULE TYPE: ORF (ii)
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:
- DHLGFISTKM RTNHGVRKGS LEEHKNLKAL GGYHYYISYF HRSDLAKLCI LSLLTFI
- (2) INFORMATION ON SEQ ID NO. 577:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 48 amino acids
    - (B) TYPE: Protein

48

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCF DESCRIPTION: SEQ ID NO: 577:
CSF CCILCKKTAN RGKRTLQIKT ILVSFPQR
(2) INFORMATION ON SEQ ID NO. 578:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 48 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(Vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:
LYFFKTLKEK CVLFAASFVR RLPTEEKGLY KLRPSWFHFH KDENKSWC 4
(2) INFORMATION ON SEQ ID NO. 579:
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 48 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

GSFPNTMICS HLCGNETKMV LICKVLFPLL AVFLQRMQQK EHIFLSKF

- (2) INFORMATION ON SEQ ID NO. 580:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 48 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

HCRILQGLSP LVGREKTTQV MRNFYSFQEL EEQLLIKFHA LVTKYFYS

4 8

- (2) INFORMATION ON SEQ ID NO. 581:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 59 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

IMPRAPLYRI PLNCNYVLLK SQLVKEELMV SVFVGNTCNT AEFYKGFLLW WAGKKPLKS 59

- (2) INFORMATION ON SEQ ID NO. 582:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 44 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:	
GTLRPRSSDV LPIYLCFTTC LLSLTPNIFT YFSNSACHKF AASP	44
(2) INFORMATION ON SEQ ID NO. 583:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 46 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:	
NVDSCQTHSL ALIPPLLSSS DIVNNDKQLL CTECFFMCCS HFIHMY	46
(2) INFORMATION ON SEQ ID NO. 584:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 41 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:	
LYMCIKCEQH IKKHSVHSSC LSLLTISLLE RRGGIRARLC V	41

- (2) INFORMATION ON SEQ ID NO. 588:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 112 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

GKPLVLHATP LSRCPLPLHP TRSLILRPSL HLSDPSFHHY LQRCSYYAPV YRGCPTMTVP 60 SQSNYSSGPK VWLSRAPLPR RGRPFQALPG WNWCRRSLGC IVRPGVGVAS LL 112

- (2) INFORMATION ON SEQ ID NO. 589:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 76 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

GRSREAPAGW PKSTKPPSAR ENPWFSMPHL SPGALCLFTP QEALSYVLLS IYRTPVSITI60 SRDVAIMRPS TGGARR 76

- (2) INFORMATION ON SEQ ID NO. 590:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 97 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

AGLDQKEELR GVRQHQHQGV RYTRGSSDTS SSPEGLGMAC HAGAMERVKA KPWDPKSNLT60 AKAPSSSGTP CRRAHNSYIS GDSDGNWGPI DGEKDVG 97

- (2) INFORMATION ON SEQ ID NO. 591:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 63 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

NGARLTSQPQ LYQRNHFIQI SQHFQRNTNV YGRVNIRSEN PLEEISVSMF IISAFRGLPV60 WAK

- (2) INFORMATION ON SEQ ID NO. 592:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 50 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

(2) INFORMATION ON SEQ ID NO. 593:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 55 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:	
AYLFIFLKGK NTFTFSSSPE AQTLLYLTTS QLTPLCDHQC GVVRLKDDSG HMTSL	55
(2) INFORMATION ON SEQ ID NO. 594:	
<ul> <li>(i) SEQUENCE CHARACTERISTIC:</li> <li>(A) LENGTH: 41 amino acids</li> <li>(B) TYPE: Protein</li> <li>(C) STRAND: individual</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: ORF	
(iii) HYPOTHETICAL: yes	
(Vi) ORIGIN (A) ORGANISM: HUMAN	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:	
SGDVCTESHC GLSRVKEKEQ QELSLGRWRR GGIDQARPWP W	41

- (2) INFORMATION ON SEQ ID NO. 595:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 47 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595: FKVGLWKGDI VEGERAVLYT YKWYTPFIHG GQRSSDQVTY VQKVTVA 47 (2) INFORMATION ON SEQ ID NO. 596: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 44 amino acids (B) TYPE: Protein (C) STRAND: individual (D) TOPOLOGY: linear (ii) MOLECULE TYPE: ORF (iii) HYPOTHETICAL: yes (vi) ORIGIN (A) ORGANISM: HUMAN (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596: SVLTTSORLS SHFKSQIPTR AKVLLDLFHP FSTSLSSTLA APSP (2) INFORMATION ON SEQ ID NO. 597: (i) SEQUENCE CHARACTERISTIC: (A) LENGTH: 1651 base pairs (B) TYPE: Nucleic acid (C) STRAND: individual (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing (iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: NO (vi) ORIGIN:

(A) ORGANISM: HUMAN

(A) LIBRARY: cDNA library

(C) ORGAN:

(vii) OTHER ORIGIN:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

```
GAGCTGCCAA GCAGCCCACC TCCTGGGCTT CCCGAAGTGG CCCCAGATGC AACCTCCACT
GGCCTCCCTG ATACCCCCGC AGCTCCAGAA ACCAGCACCA ACTACCCAGT GGAGTGCACC 120
GAGGGGTCTG CAGGCCCCCA GTCTCTCCCC TTGCCTATTC TGGAGCCGGT CAAAAACCCC 180
TGCTCTGTCA AAGACCAGAC GCCACTCCAA CTTTCTGTAG AAGATACCAC CTCTCCAAAT 240
GCGCCGTCAT CTACTCCTTG TTCAGCTCAC CTGACCCCCT CCTCCCTGTT CCCTTCCTCC 360
CTGGAATCAT CATCGGAACA GAAATTCTAT AACTTTGTGA TCCTCCACGC CAGGGCAGAC 420
GAACACATCG CCCTGCGGGT TCGGGAGAAG CTGGAGGCCC TTGGCGTGCC CGACGGGGCC 480
ACCTTCTGCG AGGATTTCCA GGTGCCGGGG CGCGGGGAGC TGAGCTGCCT GCAGGACGCC 540
ATAGACCACT CAGCTTCAT CATCCTACTT CTCACCTCCA ACTTCGACTG TCGCCTGAGC 600
CTGCACCAGG TGAACCAAGC CATGATGAGC AACCTCACGC GACAGGGGTC GCCAGACTGT 660
GTCATCCCCT TCCTGCCCCT GGAGAGCTCC CCGGCCCAGC TCAGCTCCGA CACGGCCAGC
CTGCTCTCCG GGCTGGTGCG GCTGGACGAA CACTCCCAGA TCTTCGCCAG GAAGGTGGCC 780
AACACCTTCA AGCCCCACAG GCTTCAGGCC CGAAAGGCCA TGTGGAGGAA GGAACAGGAC 840
ACCCGAGCCC TGCGGGAACA GAGCCAACAC CTGGACGGTG AGCGGATGCA GGCGGCGGCA 900
CTGAACGCAG CCTACTCAGC CTACCTCCAG AGCTACTTGT CCTACCAGGC ACAGATGGAG 960
CAGCTCCAGG TGGCTTTTGG GAGCCACATG TCATTTGGGA CTGGGGCGCC CTATGGGGTC1020
AGAATGCCCT TTGGGGGCCCA GGGGCCCCTG GGAGCCCCGC CACCCTTTCC CACTTGGCCG1080
GGGTGCCCGC AGCCGCCACC CCTGCACGCA TGGCAGGCTG GCACCCCCC ACCGCCTCC1140
CCACAGCCAG CAGCCTTTCC ACAGTCACTG CCCTTCCCGC AGTCCCCAGC CTTCCCTACG1200
GCCTCACCCG CACCCCCTCA GAGCCCAGGG CTGCAACCCC TCATTATCCA CCACGCACAG1260
ATGGTACAGC TGGGGCTGAA CAACCACATG TGGAACCAGA GAGGGTCCCA GGCGCCCGAG1320
GACAAGACGC AGGAGGCAGA ATGACCGCGT GTCCTTGCCT GACCACCTGG GGAACACCCC1380
TGGACCCAGG CATCGGCCAG GACCCCATAG AGCACCCCGG TCTGCCCTGT GCCCTGTGGA1440
CAGTGGAAGA TGAGGTCATC TGCCACTTTC AGGACATTGT CCGGGAGCCC TTCATTTAGG1500
ACAAAACGGG CGCGATGATG CCCTGGCTTT CAGGGTGGTC AGAACTGGAT ACGGTGTTTA1560
CAATTCCAAT CTCTCTATTT CTGGGTGAAG GGTCTTGGTG GTGGGGGTAT TGCTACGGTC1620
TTTTAATTAT AATAAATATT TATTGAATGC T
```

## (2) INFORMATION ON SEQ ID NO. 598:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3304 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN

**GGAT** 

## (C) ORGAN:

### (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

AAACCCTCTT GGCTGTCTGC TGTCCAGGGA GTCGCCACTC CCTTCATTAT AGCCTTGCTC

AGAGTGCAGC GGCAGGCCTG GGGATGGCCT CGGGAGAGGG ACCACAGAGC ACCAGCCTGC 120 ATGGAACTTC CTTCCTCACT CAGCTTCCCA CGTTGCCAGC TGGGACAGGG GAGATGGAGT' 180 AATTTTGCTG TGGAAAGACT TCACGTCTTG CCGAATGAAA GTCCCGCCTG TCTGTCACGC 240 TGATGCCCGT GCAGCTGTCT GAGCACCCGG AATGGAATGA GTCTATGCAC TCCCTCCGGA 300 TCAGTGTGGG GGGCCTTCCT GTGCTGGCGT CCATGACCAA GGCCGCGGAC CCCCGCTTCC 360 GCCCCGCTG GAAGGTGATC CTGACGTTCT TTGTGGGTGC TGCCATCCTC TGGCTGCTCT 420 GCTCCCACCG CCCGGCCCCC GGCAGGCCCC CCACCCACAA TGCACAAC TGGAGGCTCG 480 GCCAGGCGCC CGCCAACTGG TACAATGACA CCTACCCCCT GTCTCCCCCA CAAAGGACAC 540 CGGCTGGGAT TCGGTATCGA ATCGCAGTTA TCGCAGACCT GGACACAGAG CCAACCGCCC 600 AAGACGAAAA CACCTGGCGC AGCGACCTGA AAAAGGGCTA CCTGACCCTG TCAGACAGTG 660 GGGACAAGGT GGCCGTGGAA TGGGACAAAG ACCATGGGGT CCTGGAGTCC CACCTGGCGG 720 AGAAGGGGAG AGGCATGGAG CTATCCGACC TGATTGTTTT CAATGGGAAA CTCTACTCCG 780 TGGATGACCG GACGGGGTC GTCTACCAGA TCGAAGGCAG CAAAGCCGTG CCCTGGGTGA 840 TTCTGTCCGA CGGCGACGGC ACCGTGGAGA AAGGCTTCAA GGCCGAATGG CTGGCAGTGA 900 AGGACGAGCG TCTGTACGTG GGCGGCCTGG GCAAGGAGTG GACGACCACT ACGGGTGATG 960 TGGTGAACGA GAACCCGGAG TGGGTGAAGG TGGTGGGCTA CAAGGGCAGC GTGGACCACG1020 AGAACTGGGT GTCCAACTAC AACGCCCTGC GGGCTGCTGC CGGCATCCAG CCGCCAGCTA1080 ACCTCATCCA TGAGTCTGCC TGCTGGAGTG ACACGCTGCA GCGCTGGTTC TTCCTGCCGC1140 GCCGCGCCAG CCAGGAGCGC TACAGCGAGA AGGACGACGA GCGCAAGGGC GCCAACCTGC1200 TGCTGAGCGC CTCCCCTGAC TTCGGCGACA TCGCTGTGAG CCACGTCGGG GCGGTGGTCC1260 CCACTCACGG CTTCTCGTCC TTCAAGTTCA TCCCCAACAC CGACGACCAG ATCATTGTGG1320 CCCTCAAATC CGAGGAGGAC AGCGGCAGAG TCGCCTCCTA CATCATGGCC TTCACGCTGG1380 ACGGGCGCTT CCTGTTGCCG GAGACCAAGA TCGGAAGCGT GAAATACGAA GGCATCGAGT1440 TCATTTAÁCT CAAAACGGAA ACACTGAGCA AGGCCATCAG GACTCAGCTT TTATAAAAAC1500 AAGAGGAGTG CACTTTTGTT TTGTTTTGTT CTTTTTGGAA CTGTGCCTGG GTTGGAGGTC1560 TGGACAGGGA GCCCAGTCCC GGGCCCCATA GTGGTGCGGG CACTGGACCC CCGGGCCCCA1620 CGGAGGCCGC GGTCTGAACT GCTTTCCATG CTGCCATCTG GTGGTGATTT CGGTCACTTC1680 AGGCATTGAC TCAAGGCCTG CCTAACTGGC TGGGTCGTTT CTTCCATCCG ACCTCGTTTC1740 TTTTCTTTCC TATGTTCTTT TGTTCAGTGA ATATCCCTAG AGCTCCTACC ATATGTCAGG1800 CCCTATGCCT CACCCTGAGA ACGCAGTGAG CATGAGGTGG ACCTGTTTGC TGGGAACCCC1860 AGGTCACCCC CTTTTCTTCC CAAACTTGGT GCCTTGGAAG AATCAGGTCC AGCCCTGAAG1920 ATCCTTGGGG AAGAAAATGT TTATGTTGCA GGGTATTGCA TGGTCACGAG TGAGGGGCAG1980 GCCCCTGGGG GACACATCTG CCCACAGCTG CACAGGCCAG GGGCACAGGC ACATCTGTTG2040 GTTCTCAGGC CTCAGATAAA ACCATCTCCG CATCATATGG CCAGTGACCG CTTTCTCCCT2100 TCAAGAAAAT TCTGTGGCTG TGCAGTACTT TGAAGTTTTA ATTATTAACC TGCTTTAATT2160 AAAGCAGTTT CCTTTCTTAT AAAGTGGAAT CACCAAATCT TATCACACAG AGCACAGTCC2220 TGTAGTTACC CAGCCCGCTC CAGCAGTGCG GGAGATTGTA AGGAAGCGGT GGCGGCTGGT2280 GAAGCAAGTC TCACATGTCG GCGTTCTTGG CCAATGGATA CAAAGATAAA GAAAATGTTG2340 CCTTTTCTA GGAACTGTCA GAAATCCTCA TGCCTTTCAA GACTTCTGTG AATGACTTGA2400 ATTTTTTATT CCCTGCCTAG GGTCTGTGAA CGAGGCCTGT CTCTTCCCTG GGGTTTCTTT2460 CCATGGCCTT TATTTCTCCT CTTCCAGTGG GAGTTTTGCA GGCTCTTCTC TGTGGAAACT2520 TCACGAGCGT TGGCTGGGCC TCGGCTTCGC TGGAGTGTAC TCCAGGGTGA AGGCAGAGTG2580 GGATTTGAGA CCCAGGTTAG GCACGACCCA GGCTGAGAAG GGACGTTTCC ATCATTCACA2640 GTGCCTCCC CACAGCAACT ACCTCACCCC GACCCCCACC CTCACTCCTA CCCCACCCG2700 CGATCGTCAG GGGTGCCACG GTGGGCCGGA GGGTGCCGGC TCTGGCTGTC CCTGTGCCGG2760 TCCCTCACAA ACCTCTCCCC CTTTGAAACT CAAGCACAGC TGCGAGGAGG GCAGCGAGGA2820 GGGACCCCTC TCTCATGGTT GTCTCTTTCC CCCGCTATGT CATAGGTAGT GGAGGAAGCG2880 AAGGAAGTGA ACGCTGAATG TGACGCATTT CTGAAGAGCT CAGCTGTCAC CGGGCATAGC2940 CTGGAAGCCC CAAGTCTGTT CTGACTTTGC CTGGCTGTCT CCTTGACCCG CCTCCTAGAT3000 CATTGTCCTT GATGTCCAGG CTGGGTCATT TAAAATAGAG ATGCAATCAG GAAGGTTGGG3060 GGACTTGGGA CTGTGGCTGA ATTGAGACCT TGCTGATGTA TTCATGTCAG CACCTGAGTC3120 ACAGCCCAGG TGCCCGGAAG CAGCCTCTTC GCATAGGCAG TGATTTGCGA TTACTTTAAA3180 GCTCACCTTT TTTCTTCCCC TCTCTGTTCG CTGCTGTCAG CATAATGATT GTGTTCCTTC3240 CCTATGGGAT CCATCTGTTT TGTAAACAAT AAAGCGTCTG AGGGAGTGTA AAAAACAGAT3300

- (2) INFORMATION ON SEQ ID NO. 599:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 878 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

- (2) INFORMATION ON SEQ ID NO. 600:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 2760 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

CACCCAACCT	GTGTTGTTGC	CGCCCGGCCC	TTNCCTCCAC	AGNTCTNCTT	NCTNCCGCCC	60
				GGGGCCGGTC		120
				CATCTCTGCC		180
				CCTCGCCTGT		240
				CCTCCAGCAG		300
				CTGGAGGCCC		360
	GGGCCACGTG			CCACCCAGTG		420
				AGCTGTGTCT		
				CTGCGGGCTG		540
					TACAGCATCC	600
CAGGAGCCCG				AACATCCCTC		660
				CCACGGGTGC		720
CCCAGAGCCG		•	*	GAGGCCGGAG		780
-				AGGGGGTGCC		840
		•		CTGCCCCAGG		900
	ACCTCCCGCG			GTGGCCTCGG		960
				TAGTGTACGA		
			•	CGGACGTGCT		
GTCCCGGCCC				ATGCCTGTGC		
				AGGCTGGGCC		
		•		TCCTCCCAGA	· ·	
	CCGGAAATGT			CAGGCTCTGC	•	
CTCTGTGAAC				CAAAAAGGGG		
				AGCCGGGGCG		
				GGCCCGCCT		
				AGTCTTTCCT		1 0
	•			GCCCTGGCAC		
				TGCTGTCCAT		
				GGCCAGGGCT		
TGCTGTCTCG	GGACTCCTGA	CCGTGGTGTG	CGTGTGTGCC	CGTCTGTGAC	TTTCTACTCAL	800
				TCAAACCCCA		
TGGAGGGGAG				GTTTTCGGTG		
AACTACTCCA	TCCCATGACC				GCCTGCTGCC1	
				CAGCCCCCAG		
TCGTTGGGAG-	GACAGGGTGG	CCCTGGGGAC	AAGAGGGAGG	AGCCCAGGGG	CTTACCTCAC2	2100
TGAGAGTGCT	CCCCAGCAGG	CATCCACTAC	CCCAGGGCCC	CCCACATGTC	ATGGCAAGGT2	160
TGGTAGTGAA	TGGGCCTGGT	TGGGAGCAGC	CCCTGGCCCA	TTGCCCACCC	ACCCATCTCA2	2220
CTATGCAATT	CGAGTTCCAA	GCAACATTTG	CTCCTGCCCT	GGGGCCAGCT	CTGCCCCAGC2	2280
CCTGAGAGGG	GTGGTGAGGC	AGCCCCCTGG	ACCCCAGAAC	CCCAGACAAG	GGGGCAGGCG2	2340
GGGGACCAGG				TAACCATAAT		
TGAACCACTT				TAATCTCCTT		
	ACCCCCCGG		TGACCTCCCC		TGATTTAACA2	
	GAGGCCTGAA				TGTAGGGCCA2	
•	TACTGTCGCT	,		AACTGGGTTT		
TTTTATTTCT	TTGGGGGCTT	TTTTTCTTGG	CAAATACTAA	AAATCTCGTC	AATGTAATTT2	700
CTGTGGTTTC	TATTCAGCTT			AATTTTAAAA		

- (2) INFORMATION ON SEQ ID NO. 601:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1021 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

```
GGCGGGGCCG CGAGAGCAGT AGGTGTTAGC AGCTTGGTCG CGACAGGGGC GCTAGGTAGA
GCGCCGGGAC CTGTGACAGG GCTGGTAGCA GCGCAGAGGA AAGGCGGCTT TTAGCCAGGT 120
ATTTCAGTGT CTGTAGACAA GATGGAATCA TCTCCATTTA ATAGACGGCA ATGGACCTCA 180
CTATCATTGA GGGTAACAGC CAAAGAACTT TCTCTTGTCA ACAAGAACAA GTCATCGGCT 240
ATTGTGGAAA TATTCTCCAA GTACCAGAAA GCAGCTGAAG AAACAAACAT GGAGAAGAAG 300
AGAAGTAACA CCGAAAATCT CTCCCAGCAC TTTAGAAAGG GGACCCTGAC TGTGTTAAAG 360
AAGAAGTGGG AGAACCCAGG GCTGGGAGCA GAGTCTCACA CAGACTCTCT ACGGAACAGC 420
AGCACTGAGA TTAGGCACAG AGCAGACCAT CCTCCTGCTG AAGTGACAAG CCACGCTGCT 480
TCTGGAGCCA AAGCTGACCA AGAAGAACAA ATCCACCCCA GATCTAGACT CAGGTCACCT 540
CCTGAAGCCC TCGTTCAGGG TCGATATCCC CACATCAAGG ACGGTGAGGA TCTTAAAGAC 600
CACTCAACAG AAAGTAAAAA AATGGAAAAT TGTCTAGGAG AATCCAGGCA TGAAGTAGAA 660
AAATCAGAAA TCAGTGAAAA CACAGATGCT TCGGGCAAAA TAGAGAAATA TAATGTTCCG 720
CTGAACAGGC TTAAGATGAT GTTTGAGAAA GGTGAACCAA CTCAAACTAA GATTCTCCGG 780
GCCCAAAGCC GAAGTGCAAG TGGAAGGAAG ATCTCTGAAA ACAGCTATTC TCTAGATGAC 840
CTGGAAATAG GCCCAGGTCA GTTGTCATCT TCTACATTTG ACTCGGAGAA AAATGAGAGT 900
AGACGAAATC TGGAACTTCC ACGCCTCTCA GAAACCTCTA TAAAGGATCG AATGGCCAAG 960
TACCAGGCAG CTGTGTCCAA ACAAAGCAGC TCACCGACTA TACCAATGAG CTGAAGCCAG1020
```

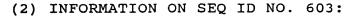
# (2) INFORMATION ON SEQ ID NO. 602:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2889 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

GATCAGGCCT GTGGTCCAGC TCACTGCCAT TGAGATTCTA GCTTGGGGCT TAAGAAATAT 60 GAAAAACTTC CAGATGGCTT CTATCACATC CCCCAGTCTT GTTGTGGAGT GTGGAGGAGA 120 AAGGGTGGAA TCGGTGGTGA TCAAAAACCT TAAGAAGACA CCCAACTTTC CAAGTTCTGT 180 TCTCTTCATG AAAGTGTTCT TGCCCAAGGA GGAATTGTAC ATGCCCCCAC TGGTGATCAA 240 GGTCATCGAC CACAGGCAGT TTGGGCGGAA GCCTGTCGTC GGCCAGTGCA CCATCGAGCG 300 CCTGGACCGC TTTCGCTGTG ACCCTTATGC AGGGAAAGAG GACATCGTCC CACAGCTCAA 360 AGCCTCCCTG CTGTCTGCCC CACCATGCCG GGACATCGTT ATCGAAATGG AAGACACCAA, 420 ACCATTACTG GCTTCTAAGC TGACAGAAAA GGAGGAAGAA ATCGTGGACT GGTGGAGTAA 480 ATTTGATGCT TCCTCAGGGG AACATGAAAA ATGCGGACAG TATATTCAGA AAGGCTATTC 540 CAAGCTCAAG ATATATAATT GTGAACTAGA AAATGTAGCA GAATTTGAGG GCCTGACAGA 600 CTTCTCAGAT ACGTTCAAGT TGTACCGAGG CAAGTCGGAT GAAAATGAAG ATCCTTCTGT 660 GGTTGGAGAG TTTAAGGGCT CCTTTCGGAT CTACCCTCTG CCGGATGACC CCAGCGTGCC 7.20 AGCCCTCCC AGACAGTTTC GGGAATTACC TGACAGCGTC CCACAGGAAT GCACGGTTAG 780 GATTTACATT GTTCGAGGCT TAGAGCTCCA GCCCCAGGAC AACAATGGCC TGTGTGACCC 840 TTACATAAAA ATAACACTGG GCAAAAAAGT CATTGAAGAC CGAGATCACT ACATTCCCAA 900 CACTCTCAAC CCAGTCTTTG GCAGGATGTA CGAACTGAGC TGCTACTTAC CTCAAGAAAA 960 AGACCTGAAA ATTTCTGTCT ATGATTATGA CACCTTTACC CGGGATGAAA AAGTAGGAGA1020 AACAATTATT GATCTGGAAA ACCGATTCCT TTCCCGCTTT GGGTCCCACT GCGGCATACC1080 AGAGGAGTAC TGTGTTTCTG GAGTCAATAC CTGGCGAGAT CAACTGAGAC CAACACAGCT1140 GCTTCAAAAT GTCGCCAGAT TCAAAGGCTT CCCACAACCC ATCCTTTCCG AAGATGGGAG1200 TAGAATCAGA TATGGAGGAC GAGACTACAG CTTGGATGAA TTTGAAGCCA ACAAAATCCT1260 GCACCAGCAC CTCGGGGCCC CTGAAGAGCG GCTTGCTCTT CACATCCTCA GGACTCAGGG1320 GCTGGTCCCT GAGCACGTGG AAACAAGGAC TTTGCACAGC ACCTTCCAGC CCAACATTTC1380 CCAGGGAAAA CTTCAGATGT GGGTGGATGT TTTCCCCAAG AGTTTGGGGC CACCAGGCCC1440 TCCTTTCAAC ATCACCCC GGAAAGCCAA GAAATACTAC CTGCGTGTGA TCATCTGGAA1500 CACCAAGGAC GTTATCTTGG ACGAGAAAAG CATCACAGGA GAGGAAATGA GTGACATCTA1560 CGTCAAAGGC TGGATTCCTG GCAATGAAGA AAACAAACAG AAAACAGATG TCCATTACAG1620 ATCTTTGGAT GGTGAAGGGA ATTTTAACTG GCGATTTGTT TTCCCGTTTG ACTACCTTCC1680 AGCCGAACAA CTCTGTATCG TTGCGAAAAA AGAGCATTTC TGGAGTATTG ACCAAACGGA1740 ATTTCGAATC CCACCCAGGC TGATCATTCA GATATGGGAC AATGACAAGT TTTCTCTGGA1800 TGACTACTTG GGTTTCCTAG AACTTGACTT GCGTCACACG ATCATTCCTG CAAAATCACC1860 AGAGAAATGC AGGTTGGACA TGATTCCGGA CCTCAAAGCC ATGAACCCCC TTAAAGCCAA1920 GACAGCCTCC CTCTTTGAGC AGAAGTCCAT GAAAGGATGG TGGCCATGCT ACGCAGAGAA1980 AGATGGCGCC CGCGTAATGG CTGGGAAAGT GGAGATGACA TTGGAAATCC TCAACGAGAA2040 GGAGGCCGAC GAGAGGCCAG CCGGGAAGGG GCGGGACGAA CCCCAACATGA ACCCCAAGCT2100 GGACTTACCA AATCGACCAG AAACCTCCTT CCTCTGGTTC ACCAACCCAT GCAAGACCAT2160 GAAGTTCATC GTGTGGCGCC GCTTTAAGTG GGTCATCATC GGCTTGCTGT TCCTGCTTAT2220 CCTGCTGCTC TTCGTGGCCG TGCTCCTCTA CTCTTTGCCG AACTATTTGT CAATGAAGAT2280 TGTAAAGCCA AATGTGTAAC AAAGGCAAAG GCTTCATTTC AAGAGTCATC CAGCAATGAG2340 AGAATCCTGC CTCTGTAGAC CAACATCCAG TGTGATTTTG TGTCTGAGAC CACACCCCAG2400 TAGCAGGTTA CGCCATGTCA CCGAGCCCCA TTGATTCCCA GAGGGTCTTA GTCCTGGAAA2460 GTCAGGCCAA CAAGCAACGT TTGCATCATG TTATCTCTTA AGTATTAAAA GTTTTATTTT2520 CTAAAGTTTA AATCATGTTT TTCAAAATAT TTTTCAAGGT GGCTGGTTCC ATTTAAAAAT2580 CATCTTTTTA TATGTGTCTT CGGTTCTAGA CTTCAGCTTT TGGAAATTGC TAAATAGAAT2640 TCAAAAATCT CTGCATCCTG AGGTGATATA CTTCATATTT GTAATCAACT GAAAGAGCTG2700 TGCATTATAA AATCAGTTAG AATAGTTAGA ACAATTCTTA TTTATGCCCA CAACCATTGC2760 TATATTTTGT ATGGATGTCA TAAAAGTCTA TTTAACCTCT GTAATGAAAC TAAATAAAAA2820 TGTTTCACCT TTAAAACATA GGGGGGGTGG TCGGGGGGGTC GGGAGGGGGG GGGGTGGTC1880 GGGGTGTGG





- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3638 base pairs
  - (B) TYPE: Nucleic acid (C) STRAND: individual

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

AGAGTTTCAG TTTTGGCAGC AGCGTCCAGT GCCCTGCCAG TAGCTCCTAG AGAGGCAGGG 60 GTTACCAACT GGCCAGCAGG CTGTGTCCCT GAAGTCAGAT CAACGGGAGA GAAGGAAGTG 120 GCTAAAACAT TGCACAGGAG AAGTCGGCCT GAGTGGTGCG GCGCTCGGGA CCCACCAGCA 180 ATGCTGCTCT TCGTGCTCAC CTGCCTGCTG GCGGTCTTCC CAGCCATCTC CACGAAGAGT 240 CCCATATTTG GTCCCGAGGA GGTGAATAGT GTGGAAGGTA ACTCAGTGTC CATCACGTGC 300 TACTACCCAC CCACCTCTGT CAACCGGCAC ACCCGGAAGT ACTGGTGCCG GCAGGGAGCT 360 AGAGGTGGCT GCATAACCCT CATCTCCTCG GAGGGCTACG TCTCCAGCAA ATATGCAGGC 420 AGGGCTAACC TCACCAACTT CCCGGAGAAC GGCACATTTG TGGTGAACAT TGCCCAGCTG 480 AGCCAGGATG ACTCCGGGCG CTACAAGTGT GGCCTGGGCA TCAATAGCCG AGGCCTGTCC 540 TTTGATGTCA GCCTGGAGGT CAGCCAGGGT CCTGGGCTCC TAAATGACAC TAAAGTCTAC 600 ACAGTGGACC TGGGCAGAAC GGTGACCATC AACTGCCCTT TCAAGACTGA GAATGCTCAA 660 AAGAGGAAGT CCTTGTACAA GCAGATAGGC CTGTACCCTG TGCTGGTCAT CGACTCCAGT 720 GGTTATGTGA ATCCCAACTA TACAGGAAGA ATACGCCTTG ATATTCAGGG TACTGGCCAA 780 CGACTGTTCA GCGTTGTCAT CAACCAACTC AGGCTCAGCG ATGCTGGGCA GTATCTCTGC 840 CAGGCTGGGG ATGATTCCAA TAGTAATAAG AAGAATGCTG ACCTCCAAGT GCTAAAGCCC 900 GAGCCCGAGC TGGTTTATGA AGACCTGAGG GGCTCAGTGA CCTTCCACTG TGCCCTGGGC 960 CCTGAGGTGG CAAACGTGGC CAAATTTCTG TGCCGACAGA GCAGTGGGGA AAACTGTGAC1020 GTGGTCGTCA ACACCCTGGG GAAGAGGGCC CCAGCCTTTG AGGGCAGGAT CCTGCTCAAC1080 CCCCAGGACA AGGATGGCTC ATTCAGTGTG GTGATCACAG GCCTGAGGAA GGAGGATGCA1140 GGGCGCTACC TGTGTGGAGC CCATTCGGAT GGTCAGCTGC AGGAAGGCTC GCCTATCCAG1200 GCCTGGCAAC TCTTCGTCAA TGAGGAGTCC ACGATTCCCC GCAGCCCCAC TGTGGTGAAG1260 GGGGTGGCAG GAGGCTCTGT GGCCGTGCTC TGCCCCTACA ACCGTAAGGA AAGCAAAAGC1320 ATCAAGTACT GGTGTCTCTG GGAAGGGGCC CAGAATGGCC GCTGCCCCCT GCTGGTGGAC1380 AGCGAGGGGT GGGTTAAGGC CCAGTACGAG GGCCGCCTCT CCCTGCTGGA GGAGCCAGGC1440 AACGGCACCT TCACTGTCAT CCTCAACCAG CTCACCAGCC GGGACGCCGG CTTCTACTGG1500 TGTCTGACCA ACGGCGATAC TCTCTGGAGG ACCACCGTGG AGATCAAGAT TATCGAAGGA1560 GAACCAAACC TCAAGGTACC AGGGAATGTC ACGGCTGTGC TGGGAGAGAC TCTCAAGGTC1620 CCCTGTCACT TTCCATGCAA ATTCTCCTCG TACGAGAAAT ACTGGTGCAA GTGGAATAAC1680 ACGGGCTGCC AGGCCCTGCC CAGCCAAGAC GAAGGCCCCA GCAAGGCCTT CGTGAACTGT1740 GACGAGAACA GCCGGCTTGT CTCCCTGACC CTGAACCTGG TGACCAGGGC TGATGAGGGC1800 TGGTACTGGT GTGGAGTGAA GCAGGGCCAC TTCTATGGAG AGACTGCAGC CGTCTATGTG1860 GCAGTTGAAG AGAGGAAGGC AGCGGGGTCC CGCGATGTCA GCCTAGCGAA GGCAGACGCT1920 GCTCCTGATG AGAAGGTGCT AGACTCTGGT TTTCGGGAGA TTGAGAACAA AGCCATTCAG1980 GATCCCAGGC TTTTTGCAGA GGAAAAGGCG GTGGCAGATA CAAGAGATCA AGCCGATGGG2040 AGCAGAGCAT CTGTGGATTC CGGCAGCTCT GAGGAACAAG GTGGAAGCTC CAGAGCGCTG2100 GTCTCCACCC TGGTGCCCCT GGGCCTGGTG CTGGCAGTGG GAGCCGTGGC TGTGGGGGTG2160 GCCAGAGCCC GGCACAGGAA GAACGTCGAC CGAGTTTCAA TCAGAAGCTA CAGGACAGAC2220 ATTAGCATGT CAGACTTCGA GAACTCCAGG GAATTTGGAG CCAATGACAA CATGGGAGCC2280 TCTTCGATCA CTCAGGAGAC ATCCCTCGGA GGAAAAGAAG AGTTTGTTGC CACCACTGAG2340 AGCACCACAG AGACCAAAGA ACCCAAGAAG GCAAAAAGGT CATCCAAGGA GGAAGCCGAG2400 ATGGCCTACA AAGACTTCCT GCTCCAGTCC AGCACCGTGG CCGCCGAGGC CCAGGACGGC2460 CCCCAGGAAG CCTAGACGGT GTCGCCGCCT GCTCCCTGCA CCCATGACAA TCACCTTCAG2520 AATCATGTCG ATCCTGGGGC CCTCAGCTCC TGGGGACCCC ACTCCCTGCT CTAACACCTG2580 CCTAGGTTTT TCCTACTGTC CTCAGAGGCG TGCTGGTCCC CTCCTCAGTG ACATCAAAGC2640 CTGGCCTAAT TGTTCCTATT GGGGATGAGG GTGGCATGAG GAGGTCCCAC TTGCAACTTC2700 TTTCTGTTGA GAGAACCTCA GGTACGGAGA AGAATAGAGG TCCTCATGGG TCCCTTGAAG2760 GAAGAGGGAC CAGGGTGGGA GAGCTGATTG CAGAAAGGAG AGACGTGCAG CGCCCCTCTG2820 CACCCTTATC ATGGGATGTC AACAGAATTT TTTCCCTCCA CTCCATCCCT CCCTCCCGTC2880 CTTCCCCTCT TCTTCTTTCC TTACCATCAA AAGATGTATT TGAATTCATA CTAGAATTCA2940 GGTGCTTTGC TAGATGCTGT GACAGGTATG CCACCAACAC TGCTCACAGC CTTTCTGAGG3000 ACACCAGTGA AAGAAGCCAC AGCTCTTCTT GGCGTATTTA TACTCACTGA GTCTTAACTT3060 TTCACCAGGG GTGCTCACCT CTGCCCCTAT TGGGAGAGGT CATAAAATGT CTCGAGTCCT3120 AAGGCCTTAG GGGTCATGTA TGATGAGCAT ACACACAGGC ATGAGCCACT GAGCCTGGCC3180 CAGAAGCGTT TTTCTCAAAG GCCCTCAGTG AGATAAATTA GATTTGGCAT CTCCTGTCCT3240 GGGCCAGGGA TCTCTCTACA AGAGCCCCTG CCCCTCTGTT GGAGGCACAG TTTTAGAATA3300 TCTGTCACTC ACATGGACCC AAGATAAAAG AATGGCCAAA CCCTCACAAC CCCTGATGTT3420 TGAAGAGTTC CAAGTTGAAG GGAAACAAAG AAGTGTTTGA TGGTGCCAGA GAGGGGCTGC3480 TCTCCAGAAA GCTAAAATTT AATTTCTTTT TTCCTCTGAG TTCTGTACTT CAACCAGCCT3540 ACAAGCTGGC ACTTGCTAAC AAATCAGAAA TATGACAATT AATGATTAAA GACTGTGATT3600

GCCACCAAAA AAAAAAAAAA AGACGAAAAG AAAAAGGG

- (2) INFORMATION ON SEQ ID NO. 604:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 2775 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

ATAGGTTTGG ACCTTTCTTG GTAGAATTAC TGCCCTAATT TTGTTCCACT GATACTAGAA 60
ACGGTCTGAT GTTAGAGCTG GAAGGGATCT GTAGTATCAC GCAGTCCGAT TCTCTAATTT 120
TCCACATGAG AAAATGAAGG TCCAGAGGAA GCAGAGACTT AACTCACAAA TCAGAAAAGC 180
GGTTCTTGCA GAACTGAGGC CATAGTGAGG ACTTTCTGCT TTCCACCATA CCACCTTGCC 240
AGTCCACACA AGAGGGAGGA TGTATTTTGG GGGGCATACA CTGAGGATGG AGAAAGATGG 300
CATCAGAACT GCTGGGTGAA GTGGTGCTT AACTGGACTT TGACAGCTGC CTTTTGAAAA 360
CCCCAAAACT AAACACACTG CATGTAATCA AAAGATGCTT ATACTAATAA TGACCTGTGC 420
TGTTCCCACT CAGTTGCTCT CTGTTTTCGA GAAGACATGA GAAGCTGCA CATGACCTGG 480
AGTGGAACTG GAGGTCACA TTTTTGTTTC AGCCACCTGC TGGCCAGCAC AGCGAGCTGCA 540
CCCTTCCCAGA AGGCTGAAGT GCTCGTGTGC TGCACCTCCC TGTGCCTCT GCAGTGGTCA 600
GAGTGACCTG GTATAAGGGA GAGGGCATCA CCTTGCCCCC TGTGCCTGCC TCACGCCCAC 720
CATGCGGGAC ATCAACAAGA AGTTCTCTGT GCGCTATTAC CTCAACCTGG TGCTGATAGA 780
CGGAGGAGGAG CGGCGCTACT TCAAGCAGCA GGAAGTGGTG TTGTGGCGGA AGGGTGACAT 840
CGTACGGAAG AGCATGTCC ACCAGGCGC CATCGCCTTC AGGGCACCAC 900

CTCCCTGGGT GAGGTGCGGA CCCCCAGCCA GCTGTCTGAC AACAACTGCA GGCAGTAGGC 960 CCCCAGGGCC GAGAAGATGC TGGGCACCCA CCCAGCACCC CCATCTACCA ACACCAGCGG1020 CTGGGGGCGG GGGCGGACCT TGTGAGGCTC AGTTGACCCG TTACTTGCAA CCTGAAAACA1080 AATCATGTTT TTGACTTAAA TTCTTTTCTC TGGAGAACCC AAGGGGCTTG GGGTGGGAAG1140 CAGTCTCTCC TTGGGATTCT GCGGCCGATG TGGGATAGAA GAGGTAGCAT CCTGGAAGCC1200 AGCCTCTCTG GGGAACATGA GCCCCCTTCC TCGGGGGGCT GCCTTGCGTC TTAGAGGAGG1260 GAGAGCAGAG AGCACGCATC CTTGGCTCCT GGCTCTCTGA GCTTCCTGAT ACAGGATCTG1320 AGCATGTCCC TGGGATTCTG AGCTGCCAAC AGGGCCCTGG GTAGTCACAT CTTGTACTCC1380 CCTTTGCTGT CCCGGAGGTA GTGGCAGGAG TTGGGCCAGC CCCCACTAAG TGGCAGGGGA1440 AGACTCACGA TTGGGAAGCT ACCTCTTTGG GAATCTTGGA TGTGGTGATC TCAAGTTCCC1500 ACAGGCCACC TCCTTCTGGC CACTCACTGC TGGGACCCAG GCACCTCCCT TCTCCATCCT1560 CTCTGGATTG TCAGTAATGT CCTGGAACAG AAGCCTGTAG GATGGCCTTG GGCACGGAGA1620 AGCCCTGGGG TCAGTGTCGT GCACGGATGG CGGCAGTGTT GAACCCAGGA GGCTGAACCC1680 GGCCCACCAC GGAAGATGAG TGCATGGCAA CCGCCTGCCT TCACGTCGCT CCACTTGGTA1740 ACCCCAAGGT CTGGGCTGTT CTAGGTATTG CTTCACGTGC CCCAGCAAGC CCTTAACAAG1800 AGGGCCTGGT TCCCTGAAGA ACCAATCCCA GGAAGGGGCC TTGATCCCTC CGCCTTGCTG1860 CGAACCTTTG GCAAGGCTGT TCTTACTAAT GCCCAAGCCC CTTTACCCCT CTCCCTATAG1980 GTTACACAGG GGAGACCAGG GCCTCGGCAG AAGACTGCTG CCACACTTCC GAATCATTCT2040 GCTTGCCAAA TAGGTCATCT TCACCAGTTG ACTGACCCAA GTTTAGGACC ATTGGTATCG2100 TGTGTTTAAA AAACACATAT AAAAAAACTC TTGTGAATAT TCTTGTTATG CTAGAGAGGA2160 AGGTACTTCT CCCTCTACGG CTCTGCGCTG GGGCCTATGG TAGTAAAGTT GTTTACTGTC2220 CTTTTTCTGC TTCCCCTGGA AATGACAGGC ATTACTCTCC CATTGGCCTC CCTTCCCTTT2280 ATAGAAAGAC CAAGCAGGCC CCACTGGCCA AGAGGTACGG TATTTGGCAG TCTGAGTTCT2340 CAGTAATTTG GAAAGTTAAG GAGTTGGTTC CTGTGTCACC TTTCAGTTAG TGTGGGAAAG2400 GAAGACTTCT GTTTTCCTGA GATCAGTGCA GTCTCAGGCC TTTGGCAGGG CTCATGGATC2460 AGAGCTGAGA CTGGAGGGAG AGGCATTTCG GGTAGCCTAG GAGGGCGACT GGCGGCAGCA2520 GAACCGAGGA AGGCAAGGTT GTTTCCCCCA CGCTGTGTCC TGTGTTCAGG TGCGACACAC2580 AATCCTCATG GGAACAGGAT CACCCATGCG CTGCCCTTGA TGATCAAGGT TGGGGCTTAA2640 GTGGATAAGG GAGGCAAGTT CTGGGTTCCT TGCCTTTTCA GAGCATGAGG TCAGGCTCTG2700 TATCCCTCCT TTTCCTAGCT GATATTCTAA CTAGAAGCAT TTGTCAAGTT CCCTGTGTGG2760 CCCTTCCCCC CAGAG

- (2) INFORMATION ON SEQ ID NO. 605:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 944 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:

- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

- (2) INFORMATION ON SEQ ID NO. 606:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1939 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

CCAGTCAAGA	ATCTCCCACT	AAGCTTCAAA	GTAGTGGATT	ACAGCATGGC	AACCATGCCA	60
GTAATTTGAA	ATTTAGTAGA	GAGGCTTTCG	CTTAGTAGAG	ATGGGTTTTT	GCAGGCTGCT	120
CCCGAACTCC	TGACCTCACC	CCACCGCGG	CAACCCCCC	ATCGGGCCCC	CAAAGTGCTG	180
GGGTTACAGG	CTTAAGCCAC	CAAGCCCGGC	CGACCTTCTT	CTATTTTTCC	ATTCTCCTTT	240
CCAAAGCCAT	GGCCATGCGC	TCCTGTGTAC	AGGTGCATAA	ACACATCAGT	GTGCCATCCC	300
TCACATGCAT	GTCGTTCCCC	ACCCCTCCTT	CCCAGGGCTT	CTCTTGGCTC	CAGCGTTCCT	360
CTGGGACCCT	CTGCAGATAC	AGCCTGTGCT	GGACCCCCAG	CCAGGGTGAG	GGCTCATTCT	420
GCTCTGTCTT	CCCCACTGCC	TCAGTTTCCC	CCAAAAGCTG	ETTTCACGTC	CTTCTAGTAG	480
GGGGCCTCCC.	ATGGGGGCAA	GGATCCCCTT	TAGGATTCAA	TCTTTCCTCT	TTGGGCAGTT	540
TTGGCTTTGA	GTCCCCCAGG	GATCAGGGTG	AGAATGAAGA	AGAGCTCAGT	GAGCGGAATG	600
ACAGCAGCTG	GGTGGGTGGT	GTGGGGAGAG	GCTGAGGGGA	AGGCAGCTCT	AAGACTGGGA	660
GTGGAGTTCC	TGGAGGTGTG	GGGAGGGGG	CGTGTTTTCA	ATTTAGAAAA	ATCTCAGCCA	720
GCTCGAGCCG	AGAGAGAATG	CGAAAGAGGA	AGTTCGGAAG	GAGCGAGGAA	TGGGGTGGGT	780
GGCAGCGGGG	GCCGCTCAGT	CGCTGTCGCT	CTTGTCCACC	AGCACGGCGT	CCGACTCCTC	840
GGTGATCTCC	AGCAGCGCGT	GCACGTCGGG	GCTGCTCCCG	CGCCGCAGGT	CGCCGGCCTC	900
CCCCCGCTCC	GCGCCGCCCT	CGTCGTCGTC	GGCGCCCACC	TCCACCATCT	CGGTGGCCTT	960
GAGCACTTCC	ACCTGGCCCT	CGCGGATCTT	CTTGACGTGG	AAGGTGAAGG	GTGGCACCTT:	1020
GTAGACCGCG	GTCTTGGAGC	GCGCGTACAC	CACGTGGTCG	GGCGTGAAGG	ATTTGCGCAA	1080
CTTGTCCCGC	GACGTCTTCA	GTTTCTCGCG	CCGCTCGGCG	GGCACCAGGC	GCGTGCCCAG	140
CTTGTTCATG	CGCTTCTCCA	GGGTGTGCCG	CGTCTTCTCC	AGGTTTTCCT	TGGTCTTGAG	200
GCGCGTCTTC	TCCAGGTTCT	CGCGGGTACG	CACCTTGGTC	TTCTCCATCT	TCTCCTTGGA1	260
GAAGGCCTTC	TTGAAGTCGT	CCACGCGCCG	CAGGCCCTGC	GCTTGATACG	CTCTGCGCGG1	.320
GACTCCTCAA	TAACCTCCTC	AACCTCCACC	GCCTCGTCCG	ACGAAAGCTC	CAGCGCCGCT1	.380
GCGTCCTCCT	CGGGCCGCTC	GCCCTCGCCC	AGCTCCTCGC	CCTCCTTCTC	TGGCAGCGCC1	440
TCCGACTCTT	TCAGCGATTT	GCTGATGCTC	AGTTTGGCCG	GCAGCTTCAC	TTCATCCTGG1	5.00
TAGATCATGA	CTTTAAAGTT	GCGGCGCCGC	AGCAGCTCGG	CCTCGTTGAC	CTCCAGCTTC1	5.60
TTGATCTGCC	CCGCCTGGCG	CTCCAGGCTG	CCGCGCACGG	TCTTCACGTT	GACGCTGACC1	.620
TTGCGCACCT	TCTCCAGCAG	CTTGCTCACC	GTATTGCTCG	TGGTGGCGTG	CGCCTTGCCC1	680
AGCTTGCTCA	GCTCGCCCTG	GATGCTCTGC	ACTGCGCCCT	CCATCTCCGC	CTGCCGCTCCI	740
TCCAGCTGTG	CTTGAGTCAG	CTGGATCTGG	TCTACGGCCC	CGATGATTTT	GTCCAGGAGG1	0,08
CTCAGCACCA	GCACGCCGTT	CACCTGGTCC	GACTTGATCA	GCTCTTCTGA	GCCGGCCCCC1	860
		AGCCCCAGCG	GAGGAAGCTC	CGGGGCCTCG	GCGATCGGGG1	920
TACCCGGGCA	AGCGGCCGC			,	1	.939

- (2) INFORMATION ON SEQ ID NO. 607:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1570 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

GGCACGAGGA AGTTAAGATC ATACATGCGG ATGTGCTGGT AACCTGCAAG AAGCAATCAT

GCTGCGGTCC	GGTGTGACCT	CCCAAGGCAT	TCACCCTGGG	AGTCCCTGGT	GCTGCACCCC	120
AACCCAGGCA,	GAGCTCATCG	TGGGTGACCA	GAGCGGGGCT	ATCCACATCT	GGGACTTGAA	180
AACAGACCAC	AACGAGCAGC	TGATCCCTGA	GCCCGAGGTC	TCCATCACGT	CCGCCCACAT	240
CGATCCCGAC	GCCAGCTACA	TGGCAGCTGT	CAATAGCACC	GGAAACTGCT	ATGTCTGGAA	300
TCTGACGGGG	GGCATTGGTG	ACGAGGTGAC	CCAGCTCATC	CCCAAGACTA	AGATCCCTGC	360
CCACACGCGC	CGTACGCCCT	GCAGTGTCGC	TTCAGCCCCG	ACTCCACGCT	CCTCGCCACC	420
TGCTCGGCCT	GATTAAGACG	GTGCAAGATC	TGGAAGGACG	TCCAACTTTC	TCCCTGATGA	480
CGGAGCTGAA	GCATCAAGAG	CGGCAACCCC	GGGGAAGTCC	TCCCGCGGCT	TGGATGTGGG	540
GGCCTGCGCT	CTCATCGGGG	GACTCCCAGT	ACATCGTCAC,	TGCTTCCTCG	GACAACCTGG	600
CCCGGCTCTG	GTGTGTGGAG	ACTGGAGAGA	TCAAGAGAGA	GTACGGCGGC	CACCAGAAGG	660
CTGTTGTCTG	CCTGGCCTTC	AATGACAGTG	TGCTGGGCTA	GCCTGTGACC	CCTCGGGACN	720
TGCCTGGTGC	AGGTGGTGGC	AGCNTGGAGG	GACCCATGCA	GCACCCAGGT	CAGAGCAGAC	780
CCNTNCCCCT	NGCCNGGCCT	GCGCCANGCT	GGNACCTGAT	GGCCCCCTGT	GGCGCCTTGA	840
CCTGCTGGGC	CAGGCTGNCC	CTGGGACTCT	CAGCCCCCAN	GTTGCTTATC	CANGATGTGA	900
CAGAGCTCGA	CCCAAGCCAG	GCTGCACACT	CCTGGACNTG	GGCTAGCCTG	CACTGCCNTG	960
GGAAAGNTCN	GCCGAGGGCC	CANAAGCTGC	TGAGGGGTNC	TGAGGCTGGT	GCCCACCCCC	L020
AAGCTAGTGT	GTTCTCTGCC	CCTCCCTGCC	CGCGTTTCAG	GGCCTCGGTC	CATAGAGAACI	1080
ACCACCACCA	TGGCCAGGTG	GAAGGGTTTA	TTAGTCCCTG	CCAGCAGCTG	TCCTCCCTGG	1140
TGCAGGTGGC	CTGGCCAGCC	CACTGGATTG	GGGACGGGCC	AGGCTGGGCC	AGGTCGGGG	1200
CTCAGTCTGG	GAGGTAATAA	AAGCAGACCG	ACACGCAGAT	GTTGCTCGGG	AAAAAAAAA	1260
AAAAAAAAA	AAAAAAAAGC	CGCTGTCTCC	GGGGCCCCTC	TGCTCGCCGG	GCCCAGTAGA	1320
TGGGGGTCCT	CATGCACAGG	CGCTGCACCA	. AAGCCCCCGC	CTGGGCGGTA	GCCACTTACG	1380
AGGCTCCCCT	GCACTGCCAG	CAGCTCCTGG	GTGTGGTGGG	TGTCCTGGCT	GGGGACCCAA	1440
GCCTCTTGGA			AGCCGCAGGT		CTGTCCTCCA	
TCAGGCGGAG	GAAGCAGACC	TGGTGCTCCT	CAGGGCGGTA	ACAGATGCAG	CCGCTCTGCC	1560
CGTCGAACAG						1570
			•			



- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1768 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
  - ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

GCACAATCCC GGCTCACTGC AACCTCCAAC TCCTGGGTTC AAGCGATTCT CCCGTCTCTA 60 CAAAGTATAC AAAAAAATTA GCCAGGCATG GTGGTGCGTG CCTGTAATCC CAGCTACTTG 120 GGAGGCTGGG GCACAGGAAT CCTTTGAACT TGGGAGGCAG AGGTTGCAGT GAGCTGAAAT 180 CACACTACTG CCCCCCAGCC TGGGCAACAG AGCAAGACTC TGTCTCGAAA AAAAAAAAAG 240 AAAACAATGA AGGAAAAGGA GGGTGAGTTA GCTGGAGTAG AATAGAGGTA TAGAATCGTT 300 CCTAAATAAC CGGCTGCATT GGTTTCCTGG AGACTTGCTA AAAACCCAGA TTCCCAGGCC 360 CCACTTCTTG GTGCTCCTAA TTCAGTAGCA TCACAGTAGG GTTCCAGAAG CGGTATTTTT 420 AACAAGCTCC CAGGTAATTC TGATGTGCAC CTAGATTTGG AAATCACTGT GTTAAAAAAT 480 ATTGTGAGGT AAGTTGGTCA GTTAGGTTGG GCAGCTTTTA TTTCATTGCT AAGGGATTTG 540 GACTTGATGG TGTAATAAAG CATTAATTGA ACAAATATTT ATGGAGCCTG TACTATGTAC 600 CAGATGCAGA CTGTGCTAGC GGTTGGGGAT ACAGTGATGA CTTGGTCTGC CTCTAGGTGG 660 CAGGGAGCCA TTTTGGGTTT TCGAACAGAA AAGTGACATA ATGAATGCTG AGTTCTTAGG 720 AAGATTAATC CAGGAGTAGT CTCCAGGATG TACTGGAAGG AGAGAAGCTG AAACCAGGGA 780 GGCTGCTGTG TTTGCAGTTG GCTGCCCAGT GCTACCTCTG CAGAGACAAT CAATGTCCTG 840 AAGGTAGCTG GTATGTCTGT GTGCACTGAC ACGAGCCTTC CTACCAAGCC CCAGGGGCTC 900 CATGCTGGAG AATGCACGTA GGGCTAGGGT GAGCACTAAC TTCACTTCAG GAGAGCAAGG 960 AACAGTGTGG CTCTTCCATT TTTCAGTTCT GTAAGCACAT CACCCTTTTC TCCTCCCCTT1020 GAGCTGTGTT CTCTGACAGC TGTTTGTTGG TAAAGCCAGC AGCCCCTAAA GCACGTCCCA1080 GCCTTGTCTC CTCTGTGCTT TCCCCCACCA CTGCTGCTGC ACGCCTCATT TGCTGGGCCA1140 CTTTAGTGGT GGAACCATTA GAGGCTGAGT GACTTAAAGG AGATTGAGTC TGTCTCGACC1200 CCGAGAGAGA GTGGGATGGA TGGATGCATC GTCTCATTTA GAAAGTGTTG CCTCTGACTC1260 TAACACACTC TTCTCTCTTT CTTTACCGCC CTCCCTGTGT GCGTCCCTGG GGGGGCGTGG1320 GCTAAACCCC TTCCGTCCCC CTTTCTCCTT CTCTCTCACA GTGTAGGCAC CACTTCTCTT1380 ACAATTTAGG CTTTCTCTCT GCCTTGGGCT GAGTGAGGAA GAGGAGTGCT GTTCCTGCCT1440 TCCTAGCCCA GCTGGGTCTG ACCAGAGGCT ACTGTGTACC CATTTACCAT GCGTGATTGT1500 TAACTCAGAG TGGGGTGTAG CCAGGTATTG ACTGAATGTA TGTTCTTGCT GACCTGTGTT1560 TTTTTCTGTA GGGACCAAAG CAGTATCCTT ACAATAATCT GTACCTGGAA CGAGGCGGTG1620 ATCCCTCCAA AGAACCAGAG CGGGTGGTTC ACTATGAGAT CTGAGGAGGC TTCGTGGGCT1680 TTTGGGTCCT CTAACTAGGA CTCCCTCATT CCTAGAAATT TAACCTTAAT GAAATCCCTA1740 ATAAAACTCA GTGCTGTGTT AAAAAAAA 1768

- (2) INFORMATION ON SEQ ID NO. 609:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1001 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

TAAGGAGACT GAAAGGTGAT TCATTTAGTG AGTAGCGATT ACAGAATTTC TAAAACAGTG GGGGCGGGG GGGCGGCGG GAGGAGGCT GGAATTGTCC TCCAGCGCAT ACAAGGTTGT 120 TGCTGCCAGA GAAATCCAGC AGGAAAGAGC AGCATTCTTT CACCTTTTCC GCCTCTGAAG 180 CGGAGGAGAA CTTCATTTCC CAGCAGCCCT TAAGATTCCT CCGCGCACTG CGTAGCGTCT 240 CCGGCATTCT GCTTTCCGGC GCTCTGCCTT CCGGTGCGTC GTTTACGGCC AGTTTGAACC 300 AAAGACGCCC AANGGTTGAG GCCGAGNTTC CAGAGCATGG GGTCTCGGTT GTCCCAGCCT 360 TTTGAGTCCT ATATCACTGC GCCTCCCGGT ACCGCCGCCG CGCCCCCAA ACCTGCGNCC 420 CCCAGCTACA CCCGGAGCGC CGACCTNCCC CNAGCAGAAC ACCGCCTNGT TGAAGANCCT 480 GCTGGAGCTG TCGNCGTNGC TTTCTGGGTT GGGGCTGATG GGGGNNCGGG CGGGTACGTG 540 TACNTGGGTG GCANCGGAAG CCCATGAAGA TNGGGATACC CCCCGAGTNC CATGGACCNA 600 TTACNGCAGA TGGTCATCGN NGCCTCANGC NATTGCCACC TNGGGGTANT CGTTGTNCAT 660 NGGCAGACCC CAAAGGGAAN GGCCTANCCG CGTTGTTTNG AAAGNTACCA CCANGTGAAT 720 NCTGTCTTCT GTCTNCTNGT CCCNTTTNCC CCGTGACACA CAGAGCAGGC ATGGAATTTA 780 ATGGGNTGTT CTGGNACNAG ACACTTGTAC ATGGACAGAC ATCACTACTN NGTGGATACT 840 NNACAAGACT GAAAAGNAAA ATCGTATGTT GTCATTCNTC TGGCTANTGG AGTGTTTGTG 900 GCCTTCACAG ATTTCACAGG AACCAATAAA TCCCTCAGAG AAGTAAAAAA NAAAAAAAA 960 А АААААААА АААААААА АААААААА АААААААА

## (2) INFORMATION ON SEQ ID NO. 610:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2515 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

GGTGTGGAAA CTACTGCAAA TAGTAGCACT TCACTGAGAT CTACAACTCT TGAAAAAGAA 60 GTTCCTGTCA TCTTCATCCA CCCTTTAAAC ACTGGATTAT TCCGGATAAA AATTCAAGGA 120 GCCACTGGAA AATTTAATAT GGTCATCCCT CTTGTGGATG GGATGATTGT CAGCAGGCGA 180 GCTCTTGGCT TTCTGGTGAG GCAGACTGTA ATTAACATTT GTAGAAGAAA GAGACTGGAA 240 AGTGACTCCT ACAGTCCCCC CATGTCCGCC GGAAACAGAA AATCACCGAC ATTGTCAACA 300 AGTACCGGAA CAAGCAGCTG GAGCCAGAGT TTTATACTTC ACTTTTCCAG GAGGTTGGAC 360 TCAAGAACTG CAGTTCTTAG ACCACTGAAT TTCTAAGACT GTTGAACTCC AGTTTGGGAA 420 CTATAACACA GCAGAACAGT TTGATAGGTG ATCACTGTAA AAATAAAAAC AAATCACTCC 480 CAAGAGCTTA CTGTTTAATC ACCAGAATAG AAGAAACACA TTATAACCCA TTTGATAGAA 540 GACTTTGGGC TATCTAGTGA AATGGGCTCC CAGACACAAT CATACTCCTG CTGATAATGA 600 TGATATACAT TTTAGCCATA AACTTTCTTT TAAAAGTGAC AATTTTAGTT AAACATAAGC 660 CTTTTGAGGA GAAAGGCTTT TATGCATCTC AGTTAAACAC GTGCATTGGT AGTATCAACA 720 AATTTGCAAT ATAGAAGTTG AAGATAGTTT TTTNCCTCAC TTTTTAGGAG GCTGTATTCA 780 AAATTAAAAT CTCAGAATCT TACAGGACAT TTAAAGGACT CATGTTGATA GCATGGAGGA 840 GAAGGAAAGA AGTCACAGCC TTCTACTCAG TTGTAGGTCT TCTTGTCATC CAGCTGTCAC 900 ACTGACAAAA AGAAAAGATG ATANCATGTT TTTTTGCTCA GATAAGAAGC CTGACATTAA 960 AAGATGTCAT ATTTTTTCT CCACATTTCA AAAAGTTGTC CTTCTCATCA CTGCACAGAT1020 CTGTCTGAAA GCCTCAGTTT CTGAGTGACC CAGGAACAGA TCAGAAATGG AGCATGGCCT1080 TGTCCTTTAA TGGGGATGCA AATAAAGTTT GTGGGGTTAA AAGTTATAAG ACAGCAGTGA1140 TACCCCACTC TCTCCATTAT TGTCCAGCGG GGTGACATAA TGACAGGTTA AATATTTGTG1200 ATTCATTGAT TAAATATTAT TTAAAGAAAT GTAAAAAAA AAAAAAGGTT GAAAATTATT1260 TGGTTTCATC CATTGTCTCT TATTTCAGGA CCAAGCAGCA AACTGCAGTA GTTTGTGAAG1320 GATTCTAATA TGGGGTTCAG GAATAGCCTC TCAACGCTAC TAATTCAGAT CTCTCCCAGA1380 GAACTACTGG ATTTCCTCAT AATTGACAAA CATGAGTGAC CACCTCTTTG GGTGGCTACT1440 GTTAGAAATG GCTGTTGTCA TGTTTTCTGG ACTTTGCCAG CCAACAGATC CCTGCCAGGT1500 TTTGGAAATA CTTCTATTAC CTCGCTGCTA CTTTTCTGCA GGGATAAAAC TTTTGNAGGT1560 GGCCAGACCC AGAACATCCA AGGATTCCTG TTACAGTGCT ACAGTATACA CTGCTCATTT1620 ATCCTATTCT CATGTGCTTT CTTCTTTAGT AAGATTATTT TAAGAAAATA AGTGATATTT1680 AAAGTCCAAA GAGGAATGAT CACAGTTGTA TAAGGGGTGT TTTCCCACTT GAACTCTGAT1740 GTCAGTCGAC TGTGGGTCAG AGCTACAACC ATCTGTTTGG TTTGATGTTT TGGTGGTTTA1800 CTTACGGAGT GGGGATAGTG TGAGACCTAA TTCCCTGTGC AAATGTCTCT TATTCCAGAA1860 ATGTGCATTT TGTCATCTAT AAGCAAGAAA TATGGGCATA GCAGCTCTTG GTTTAAANGT1920 TTGCCATAAC CTGTTCATGT TTGTTTTAAG CTCAGGTAAA GATAACCTCC NTCTTTCTAT1980 GACTCCAGTT TCCATTCAGG TTATAGTATT ATTCAATAGT TGATTTTCTT TTTAAGCTNG2040 GGCAATAAAT TGATGTTTCC AGATGGTAAC ATGGGANGAG GGCATATAGG ATAAAGATNG2100 AGCAAATTCT ACCCTAAAAA TGNTTCTAGT AGTTCACAGG AAGAAGATGA GGTTTAATAA2160 CTTTCAAGGT AATTCTAGAT TGACATTTTN GAGGGGAAAA TGGGCTCTTG TTCTAGTTGA2220 AGTGAGCAGA GAANGGCTAT NAAATTAATA TGTAANCTTA CAGCATTCCA GAGGTTAAAA2280 ATAACTGATG CAGATGTACT TCTTCAGTGT GATTCTTCAG ATCAAACTTT TACTTTTGGC2340 ATAGTTAATT TCAGAAAAAT GTGCTGTATG TGTGTGTGTA TGAGGGTTGG TCTTGCTGAT2400 CCTTCAGTTA GCTCTAAATT CTGGCAACTC CTTGTAATTC CCATGTATTT GATACCATGA2460 -----

### (2) INFORMATION ON SEQ ID NO. 611:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 818 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
    - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

TTTTTTTTT ATTTAAAGCC TGGATTGTAA CCAGATTTC TTTTTCCCC CTTCCAGCT 60
GTAGATATGA TATCTCCTTT CAGGGCCCCA GCTTAAGGGC AAAGTGAGTT AATGTGTAGA120
CAAAGGCGAG GGACAAGAG GAGTTAACAT CTAGACAGTG GAAAAAGCCA TGGTGTGTG180
TTTCTGGGAA CCACCAACAC TTGCAGGTTT AGCTTTTCC CAGGGTTGAC TACAAGAAAG240
AAAACCATGT TTTTGCAAGA TTAAAATGTG GTTGAGTGT CCTAAATTAA CCATCCCCAT300
TTTTATCATA TTTCCACCAT CACTTCAGGG TTTTAAGAGT CAGTGCTCAC CTGGGCGGAG360
CTGGTAGTAC ATTTTGCTTC TTAGAAAGCT AAGTCCTGGG TTCCGTCTGA TTTTAGGTTC420
CAGGAACTTC CTGAGAACAC CCGATCGCAG AGGGTAATTT TCTGGAGTTT GTTTTGCAGG480
GATAGCTGGG AGTATGGCCA CCCTGCTCCA CGATGCGGTA ATGAATCCAG CAGAAGTGGT540
GAAGCAGCGC TTGCAGATGT ACAACTCGCA GCACCGGTCA GCAATCAGCT GCATCCGGAC600
GGTGTGGAGG ACCGAGGGGT TGGGGGCCTT CTACCGGAGC TACACCACGC CAGCTGACCA660
TGAACATCCC CTTCCAGTCC ATCCACTTCA TCACCTATGA GTTCCTGCAG GAGCAGGTCA720
ACCCCCACCG GACCTACAAC CCGCAGTCCC ACATCATCT AGGCGGGCTG GCCGGGGCCC780
TTGCCGCGGC GGCGAGGGC CCCCTGGACC TTTTTAAGA 818

- (2) INFORMATION ON SEQ ID NO. 612:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1024 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual

ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

GCGGTCGGTA GTGCGGCGCT GTTTAAAGAT GGCGGCGGAG GAACCTCAGC AGCAGAAGCA GGAGCCGCTG GGCAGCGACT CCGAAGTGTT AACTGTCTGG CCTATGATGA AGCCATCATG 120 GCTCAGCAGG ACCGAATTCA GCAAGAGATT GCTGTGCAGA ACCCTCTGGT GTCAGAGCGG 180 CTGGAGCTCT CGGTCCTATA CAAGGAGTAT GCTGAAGATG ACAACATCTA TCAACAGAAG 240 ATCAAGGACC TCCACAAAAA GTACTCGTAC ATCCGCAAGA CCAGGCCTGA CGGCAACTGT 300 TTCTATCGGG CTTTCGGATT CTCCCACTTG GAGGCACTGC TGGATGACAG CAAGGAGTTG 360 CAGCGGTTCA AGGCTGTGTC TGCCAAGAGC AAGGAAGACC TGGTGTCCCA GGGCTTCACT 420 GAATTCACAA TTGAGGATTT CCACAACACG TTCATGGACC TGATTGAGCA GGTGGAGAAG 480 CAGACCTCTG TCGCCGACCT GCTGGCCTCC TTCAATGACC AGAGCACCTC CGACTACCTT 540 GTGGTCTACC TGCGGCTGCT CACCTCGGGC TACCTGCAGC GCGAGAGCAA GTTCTTCGAG 600 CACTICATCG AGGGTGGACG GACTGTCAAG GAGTTCTGCC AGCAGGAGGT GGAGCCCATG 660 TGCAAGGAGA GCGACCACAT CCACATCATT GCGCTGGCCC AGGCCCTCAG CGTGTCCATC 720 CAGGTGGAGT ACATGGACCG CGGCGAGGGC GGCACCACCA ATCCGCACAT CTTCCCTGAG 780 GGCTCCGAGC CCAAGGTCTA CCTTCTCTAC CGGCCTGGAC ACTACGATAT CCTCTACAAA 840 TAGGGCTGGC TCCAGCCCGC TGCTGCCCTG CTGCCCCCT CTGCCAGGCG CTAGACATGT 900 ACAGAGGTTT TTCTGTGGTT GTAAATGGTC CTATTTCACC CCCTTCTTCC TGTCACATGA 960 

## (2) INFORMATION ON SEQ ID NO. 613:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1322 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

GCTGACCACG	ACATGTGTCT	CCTCCTCTGC	ACCTTCCAAG	ACCTCCTTAA	TAATGAACCC	60
	ACCAATGGAC	AGCTCTCAGT	CCACACTCCC	AAAAGGGAAA	GTTTGTCCCA	120
	CCCCATAGCC	ATCCTCTCTA	TGGACATGGT	GTATGCAAGT	GGCCAGGCTG	180
TGAAGCAGTG	TGCGAAGATT	TCCAATCATT	TCTAAAACAT	CTCAACAGTG	AGCATGCGCT	240
GGACGATAGA	AGTACAGCCC	AATGTAGAGT	ACAAATGCAG	GTTGTACAGC	AGTTAGAGCT	300
ACAGCTTGCA	AAAGACAAAG	AGCGCCTGCA	AGCCATGATG	ACCCACCTGC	ATGTGAAGTC	360
TACAGAACCC	AAAGCCGCCC	CTCAGCCCTT	GAATCTGGTA	TCAAGTGTCA	CTCTCTCCAA	420 -
GTCCGCATCG	GAGGCTTCTC	CACAGAGCTT	ACCTCATACT	CCAACGACCC	CAACCGCCCC	480
CCTGACTCCC	GTCACCCAAG	GCCCCTCTGT	CATCACAACC	ACCAGCATGC	ACACGGTGGG	540
ACCCATCCGC	AGGCGGTACT	CAGACAAATA	CAACGTGCCC	ATTTCGTCAG	CAGATATTGC	600
GCAGAACCAA	GAATTTTATA	AGAACGCAGA	AGTTAGACCA	CCATTTACAT	ATGCATCTTT	660
AATTAGGCAG	GCCATTCTCG	AATCTCCAGA	AAAGCAGCTA	ACACTAAATG	AGATCTATAA	720
CTGGTTCACA	CGAATGTTTG	CTTACTTCCG	ACGCAACGCG	GCCACGTGGA	AGAATGCAGT	780
GCGTCATAAT	CTTAGTCTTC	ACAAGTGTTT	TGTGCGAGTA	GAAAACGTTA	AAGGGGCAGT	840
ATGGACAGTG	GATGAAGTAG	AATTCCAAAA	ACGAAGGCCA	CAAAAGATCA	GTGGTAACCC	900-
TTCCCTTATT	AAAAACATGC	AGAGCAGCCA	CGCCTACTGC	ACACCTCTCA	ATGCAGCTTT	960
ACAGGCTTCA	ATGGCTGAGA	ATAGTATACC	TCTATACACT	ACCGCTTCCA	TGGGAAATCC1	.020
CACTCTGGGC	AACTTAGCCA	GCGCAATACG	GGAAGAGCTG	AACGGGGCAA	TGGAGCATACI	080
CAACAGCAAC	GAGAGTGACA	GCAGTCCAGG	CAGATCTCCT	ATGCAAGCCG	TGCATCCTGT1	140
ACACGTCAAA	GAAGAGCCCC	TCGATCCAGA	GGAAGCTGAA	GGGCCCCTGT	CCTTAGTGACI	200
AACAGCCAAC		ATTTTGACCA	TGACAGAGAT	TACGAAGATG	AACCAGTAAA1	260
CGAGGACATG		CGGGGCGGC	CAACCCCGAG	AATGAAGATT	GGAAAAAGGA1	1320
AA					1	.322

- (2) INFORMATION ON SEQ ID NO. 614:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 4458 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

GCCCGGCGTT	AACAAAGGGA	GCCGATACCG	ACCGGCGTGG	GCGCGGAGCG	GGCGGCCGCC	60
ACCGAGCGTG	CTGAGCAACC	GCAGCCTCCG	CGGCCGAGAG	TGCAGCGAGC	AAGGGGACAA	120
AAACTTCCCC	ANAGECEGEA	CAACCAGCAC	CACAGAGAGA	AGGGAAGAAC	GGCATCCAGC	180
AAAGIICCGC	TCCACCCACA	CACCTCAGCA	TCTCCAAACC	CCGCAGCACA	CGTGACCATA	240
CCACCAGAAA	CARCACTETT	CACCICACCA	AGAAAAATGG	GCCTTGGCCT	GCAGACCCAA	300
AACCAGCAAA	GATGAGITII	GAICAICCIG	AUDALANTIOG	CACCTGAAGG	GCCTGCCGCC	360
TAAACCTTCC	CTCCCATGGA	TAATAGTGCT	AATICCIGAG	CARCIGARGO	GCCTGCCGCC	420
CCTGGGGGAT	TAGCCAGAAG	CAGGCTTGTT	TICCIGCICA	GAACAAAGIG	ACTTCCCTGA	420
ACACATCTTC	ATTATGATTC	ACACCAACCT	GAAGAAAAAG	TTCAGCTGCT	GCGTCCTGGT	400
CTTTCTTCTG	TTTGCAGTCA	TCTGTGTGTG	GAAGGAAAAG	AAGAAAGGGA	GTTACTATGA	540
TTCCTTTAAA	TTGCAAACCA	AGGAATTCCA	GGTGTTAAAG	AGTCTGGGGA	121110000	600
CCCCTCTCAT	TCCCAGTCTG	TATCCTCAAG	CAGCACCCAG	GACCCCCACA	GGGGCCGCCA	660
CACCCTCGGC	AGTCTCAGAG	GCCTAGCCAA	GGCCAAACCA	GAGGCCTCCT	TCCAGGTGTG	720
CARCATOGAC	AGCTCTTCCA	AAAACCTTAT	CCCTAGGCTG	CAAAAGATCT	GGAAGAATTA	780
<b>つれむひれれつれれむ</b>	TOCTOT FOOL					

CCTAAGCATG AACAAGTACA AAGTGTCCTA CAAGGGGCCA GGACCAGGCA TCAAGTTCAG 840 TGCAGAGGCC CTGCGCTGCC ACCTCCGGGA CCATGTGAAT GTATCCATGG TAGAGGTCAC 900 AGATTTTCCC TTCAATACCT CTGAATGGGA GGGTTATCTG CCCAAGGAGA GCATTAGGAC 960 CAAGGCTGGG CCTTGGGGCA GGTGTGCTGT TGTGTCGTCA GCGGGATCTC TGAAGTCCTC1020 CCAACTAGGC AGAGAAATCG ATGATCATGA CGCAGTCCTG AGGTTTAATG GGGCACCCAC1080 AGCCAACTIC CAACAAGATG TGGGCACAAA AACTACCATT CGCCTGATGA ACTCTCAGTT1140 GGTTACCACA GAGAAGCGCT TCCTCAAAGA CAGTTTGTAC AATGAAGGAA TCCTAATTGT1200 ATGGGACCCA TCTGTATACC ACTCAGATAT CCCAAAGTGG TACCAGAATC CGGATTATAA1260 TTTCTTTAAC AACTACAAGA CTTATCGTAA GCTGCACCCC AATCAGCCCT TTTACATCCT1320 CAAGCCCCAG ATGCCTTGGG AGCTATGGGA CATTCTTCAA GAAATCTCCC CAGAAGAGAT1380 TCAGCCAAAC CCCCCATCCT CTGGGATGCT TGGTATCATC ATCATGATGA CGCTGTGTGA1440 CCAGGTGGAT ATTTATGAGT CCCTCCCATC CAAGCGCAAG ACTGACGTGT GCTACTACTA1500 CCAGAAGTTC TTCGATAGTG CCTGCACGAT GGGTGCCTAC CACCCGCTGC TCTATGAGAA1560 GAATTTGGTG AAGCATCTCA ACCAGGGCAC AGATGAGGAC ATCTACCTGC TTGGAAAAGC1620 CACACTGCCT GGCTTCCGGA CCATTCACTG CTAAGCACAG GCTCCTCACT CTTCTCCATC1680 AGGCATTAAA TGAATGGTCT CTTGGCCACC CCAGCCTGGG AAGAACATTT TCCTGAACAA1740 TTCCAGCCTG CTCCTTTTAC TCTAGGGGCC TCTGTCAGCA AGACCATGGG GACTTCAAGA1800 GCCTGTGGTC AGGAAATCAG GTCCAGCCTT CCCTGTAGCC AGACAGTTTA TGAGCCCAGA1860 GCCTCCTGCC ACACACATGC ACACATATCT AGCATTCTTT CCAGACAGCA TCCTCCCCGC1920 CTTCCACCTT GGTAGATGCA AGGTCTATCT CTCCCATCAG GGCTGCCAAA GCTGGGCTTT1980 GTTTTTCCCA GCAGAATGAT GCCATTCTCA CAAACCAATG CTCTATATTG CTTNGAAGTC2040 TGCATCTAAA TATTGATTTC ACGNTTTTAA AGNAAATTCT NNCTTAAATT ACAATTGTGC2100 CCAATGCAGG GTGGNCTCTN NGGGGGGCAA GTAGGTGGTA CAGGGGATTG GAAACATCCT2160 CCGCGCCTCC AGAGAAAAGT TGCTCCCGAG GTCCATGCCC CTGGAACGTG TTCCTATCAC2220 TCTGGCTGGT TGGGCTGGTC CTTAGACTGG GTGCTTATGA TTAAAAGGGT CTTGGTTAAG2280 CCCACTTTCC CTCTCCATGT GGAGATGGAA GGTAGAGAAG GATACAGTGT CTATCCTCAA2340 GTTGCTACGG TTCAGTGAGA GAGGCAGACA TCTGAACAGG NCAGGTAGGA TTCAGTGTGC2400 TCAGTGCACT GGGGATTTGG AGAGAGATGG GCTTGCTCTC TCTGTGCACC CAGGAGGGCC2460 ACGCACTTAA AACTGTGTTT GTGGATCAGA GAAGGCTTTA TAGCACAGGG GGCATTCAGA2520 TGAGTCTTAG AGGAAGAGA GAAACATGGC AAGCAGATTA CATCTGAGCC GTTTGAATTG2580 TGTTTTCTT TCTTCCCATG TTTATTTTCT AAGATCTACC TGAACTTAGN AGACTCAAGA2640 TATTTTTTTA GGAAACCTCC TACCCATGTC TGAGGTAGCA AGTGCAGCCT CACGACAGAT2700 ACCAGGCAAT CCAGAGCCAC AAAACGTGAT TCCTCCAGGC TCTGCCTGGC CTGACCCTGT2760 CCTGTCAGCT GGGTTTACAT ACCAGTCCCA TTCTTCCTTT TCAATACCTA CCCCCAAATC2820 TTCTCCTAAC CACCATCTGT TTTTTTTAG TTAAAGCATT TTTTGCTTTA AAAGCATCCT2880 GACCCCAATT TCTTTGAGCT CACGGGCCTT TTGCTGAAGG TCTCTCAGGG TGTAGTGGTG2940 TGGCTCTCTG GACTTAACGT CACTCTCAGN AGGTCAGAAC CTTNGGAGAT CAGAACTGAT3000 TCTCACCAGG TGTGAGAGGT GTGGNTANGC AGATTGCAAT GCTCTGCACC TCTTNCCTTG3060 CAAGTGAGNC AACTTNCAGG NCTCTCTGGG NCAGAGGCTG GCCCACTGTA GTTTGCAGAC3120 ATGCTCTCCA GATGGNTTTT ACTAAGTCCC CTCTCCCTGN ATANGGGAAT CCTGNCTGGN3180 ACCAGCGCAN GCCCTNNGGT GTNGGANNGA GGTTNAAAAG ACTTGNCACA GGNATCACCA3240 AGTNCATGCT GNTAGANGCC AGGATTCCTA GACCCAGGGC TCTGCACTCT CAAGGCTGGC3300 CCCATGTGCT CAAGGGGGTC TAATGTTTGG GCTCCAAACT AACCATCTCG GAGCTGGGCT3360 CCTCATTTAC TGCCAAACCC TCAGNCTTAT GTAGCNTAGA AAGGGCCCTG GANGTGNAGA3420 AAGCCTGGAT TTTCAAATTG ATGCTCCCCT ACTNGACTAG NCTGTGCCAC TCNTGGGCAA3480 ATGCTCTTCC TTGAGCCTGT TTCCACACCT GTAAAGTGGG GATGATGATC CTATCTCACT3540 GCTTTTNGTG NAGGATTACA GGNNAAAGCA CCTGTCCTGG CTCTGTACCT GGCACGTAGT3600 ANGGTGCTCA GTTCATGCTG GTTTCCTTCC TGCCTTTAGT AGGGACCTGC TCTGTGCTCA3660 CACCTCGGCT GCATGCACCC TGCTGTGACG GAGGCTAGTG TGGAAGAGGT CCTGTCCTCA3720 GGGAATTAAC TGTCTTATTG GGAGACAACA ACTGTCCTCC TTGGAACACC CAAGAAACCA3780 TGNCAAAGCA GTGGACAACA CAGAACACGN CCCTCCTCCT CGCTGCCTGC AGCTNCCAAT3840 CTGATTCTGC TTGGGAATGG GCGGANCACG NTGGGCTGCT TAACTGCTGT ATAGGACAAG3900 CCCCTTACCC CTCTCTGGGC CCATGAATTC CTGGCTTGGT TTATGTTCTG ATTTGACACA3960 CTGATTTTAA TCTTCGAATC ATGACACTGA GTGCAGAGGA GGTGGCATTC CGACAGCAGG4020 ACATACATGT TNGGTGTGAA GACTGGGACG ACACTGGGTA GAATCTAGTT TTTAATTATT4080 ATTAATATAA AGGATCAAAT TAATTTAAAT ATGAATCTGA AGTCCACAGA ACTTTNNNNN4140 AAGTGCTGTC CAGGCCAACA CTTTGGTAAA ATGCAAATTA TGATATGGAC GTTATCATTG4200 GTCTGGTGAG ATGTTTCATA TTTGTGACAG TTAATTTAAA AATTATGACT TAATGCTGCC4260 TGTGTCTATG GGGTTCTGTC TTCTTTGATA GCCATCTATT CATCTGGATC ATGGGACCCT4320 CTCTAATCCT TCCACCAATC AAATAAGCTA TTGCTATTGG TTTGGAGTTG AGATATCAGT4380 CTCGGAAACT TCTGAAAAAT GCTAATAATT ACCCAAGGAT TATGTCAAAT TTTAAAATAA4440 ATGTGTGTGT GTTTCTTT

- (2) INFORMATION ON SEQ ID NO. 615:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 1562 base pairs
    - (B) TYPE: Nucleic acid
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGIN:
    - (A) ORGANISM: HUMAN
    - (C) ORGAN:
  - (vii) OTHER ORIGIN:
    - (A) LIBRARY: cDNA library
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

TGGAGGCAGC TAGCGCGAGG GTGGGGAGCG CTGAGCCGCG CGTCGTGCCC TGCGCTGCCC 60 AGACTAGCGA ACAATACAGT CAGGATGGCT AAAGGTGACC CCAAGAAACC AAAGGGCAAG 120 ATGTCCGCTT ATGCCTTCTT TGTGCAGACA TGCAGAGAAG AACATAAGAA GAAAAACCCA 180 GAGGTCCCTG TCAATTTTGC GGAATTTTCC AAGAAGTGCT CTGAGAGGTG GAAGACGATG 240 TCCGGGAAAG AGAAATCTAA ATTTGATGAA ATGGCAAAGG CAGATAAAGT GCGCTATGAT 300 CGGGAAATGA AGGATTATGG ACCAGCTAAG GGAGGCAAGA AGAAGAAGGA TCCTAATGCT 360 CCCAAAAGGC CACCGTCTGG ATTCTTCCTG TTCTGTTCAG AATTCCGCCC CAAGATCAAA 420 TCCACAAACC CCGGCATCTC TATTGGAGAC GTGGCAAAAA AGCTGGGTGA GATGTGGAAT 480 AACTTAAATG ACAGTGAAAA GCAGCCTTAC ATCACTAAGA CGGCAAAGCT GAAGGAGAAG 540 TACGAGAAGG ATGTTGCTGA CTATAAGTCG AAAGGAAAGT TTGATGGTGC AAAGGGTCCT 600 GCTAAAGTTG CCCGGAAAAA GGTGGAAGAG GAAGATGAAG AAGACGGGGG GGGGGGGGG 660 GGGGGGGGG GGGGGACGTA TAGTCGGGTC GGCTGGTGGA GTAGCCCAAA AGAAGGGGAG 720 CGCCGTAATT GACACATCTC TTATTTGAGA AGTGTCTGTT GCCCTCATTA GGTTTAATTA 780 CAAAATTTGA TCACGATCAT ATTGTAGTCT CTCAAAGTGC TCTAGAAATT GTCAGTGGTT 840 TACATGAAGT GGCCATGGGT GTCTGGAGCA CCCTGAAACT GTATCAAAGT TGTACATATT 900 TCCAAACATT TTTAAAATGA AAAGGCACTC TCGTGTTCTC CTCACTCTGT GCACTTTGCT 960 GTTGGTGTGA CAAGGCATTT AAAGATGTTT CTGGCATTTT CTTTTTATTT GTAAGGTGGT1020 GGTAACTATG GTTATTGGCT AGAAATCCTG AGTTTTCAAC TGTATATATC TATAGTTTGT1080 AAAAAGAACA AAACAACCGA GACAAACCCT TGATGCTCCT TGCTCGGCGT TGAGGCTGTG1140 GGGAAGATGC CTTTTGGGAG AGGCTGTAGC TCAGGGCGTG CACTGTGAGG CTGGACCTGT1200 TGACTCTGCA GGGGGCATCC ATTTAGCTTC AGGTTGTCTT GTTTCTGTAT ATAGTGACAT1260 AGCATTCTGC TGCCATCTTA GCTGTGGACA AAGGGGGGTC AGCTGGCATG AGAATATTTT1320 TTTTTTTAAG TGCGGTAGTT TTTAAACTGT TTGTTTTTAA ACAAACTATA GAACTCTTCA1380 TTGTCAGCAA AGCAAAGAGT CACTGCATCA ATGAAAGTTC AAGAACCTCC TGTACTTAAA1440 CACGATTCGC AACGTTCTGT TATTTTTTTT GTATGTTTAG AATGCTGAAA TGTTTTTGAA1500 1562 AA

#### (2) INFORMATION ON SEQ ID NO. 616:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2278 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

GGCAATTTCC GTTAGGTGCT GAAGGCTGTG GCGCGCGGCT GTCCCCATTC CCACGTGAAG 60 CGCTACGCTA GCATCGCTCG GCTGGCGGCT CCCAGCTCGC CGCGGAGCAG TCCCGGCAGC 120 AGCGGGGGAC CGGAAGTGGC TCGCGGAGGC TCAGAAGCTA GTCCCGGAGC CCGGCGTGTG 180 GCGCCTCGGA GCACGGTGAC GGCGCCATGT CCCTAATCTG CTCCATCTCT AACGAAATGC 240 CGGAGCACCC ATGTGTATCC CCTGTCTCTA ATCATGTTTA TGAGCGGCGG CTCATCGAGA 300 AGTACATTGC GGAGAATGGT ACCGACCCCA TCAACAACCA GCCTCTCTCC GAGGAGCAGC 360 TCATCGACAT CAAAGTTGCT CACCCAATCC GGCCCAAGCC TCCCTCAGCC ACCAGCATCC 420 CGGCCATTCT GAAAGCTTTG CAGGATGAGT GGGATGCAGT CATGCTGCAC AGCTTCACTC 480 TGCGCCAGAG CTGCAGACAA CCCGCCAAGA GCTGTCACAC GCTCTGTACC AGCACGATGC 540 CGCCTGCCGT GTCATTGCCC GTCTCACCAA GGAAGTCACT GCTGCCCGAG AAGCTCTGGC 600 TACCCTGAAA CCACAGGCTG GCCTCATTGT GCCCCAGGCT GTGCCAAGTT CCCAACCAAG 660 TGTTGTGGGT GCGGGTGAGC CAATGGATTT GGGTGAGCTG GTGGGAATGA CCCCAGAGAT 720 TATTCAGAAG CTTCAAGACA AAGCCACTGT GCTAACCACG GAGCGCAAGA AGAGAGGGAA 780 GACTGTGCCT GAGGAGCTGG TGAAGCCAGA AGAGCTCAGC AAATACCGGC AGGTGGCATC 840 CCACGTGGGG TTGCACAGTG CCAGCATTCC TGGGATCCTG GCCCTGGACC TCTGCCCGTC 900 CGACACCAAC AAGATCCTCA CTGGTGGGGC GGATAAAAAT GTCGTTGTGT TTGACAAAAG 960 TTCTGAACAA ATCCTGGCTA CCCTCAAAGG CCATACCAAG AAGGTCACCA GCGTGGTGTT1020 TCACCCTTCC CAGGACCTGG TGTTTTCTGC TTCCCCCGAT GCCACTATCA GGATTTGGTC1080 GGTCCCCAAT GCCTCTTGTG TACAGGTGGT TCGGGCCCAT GAGAGTGCTG TGACAGGCCT1140 CAGCCTTCAT GCCACTGGCG ACTATCTCCT GAGCTCCTCC GATGATCAGT ACTGGGCTTT1200 CTCTGACATC CAGACAGGGC GTGTGCTCAC CAAGGTGACA GATGAGACCT CCGGCTGCTC1260 TCTCACCTGT GCACAGTTCC ACCCTGACGG ACTCATCTTT GGAACAGGAA CCATGGACTC1320 TCAGATCAAG ATCTGGGACT TGAAGGAACG TACTAATGTG GCCAACTTCC CTGGCCACTC1380 GGGCCCCATC ACTAGCATCG CCTTCTCTGA GAATGGTTAC TACCTGGCTA CAGCGGCTGA1440 TGACTCCTCT GTCAAGCTCT GGGATCTGCG CAAGTTAAGA ACTTTAAGAC TTTGCAGCTG1500 GATAACAACT TTGAGGTAAA GTCACTGATC TTTGACCAGA GTGGTACCTA CCTGGCTCTT1560 GGGGGCACGG ATGTCCAGAT CTACATCTGC AAACAATGGA CGGAGATTCT TCACTTTACA1620 GAGCATAGCG GCCTGACCAC AGGGGTGGCC TTCGGGCATC ACGCCAAGTT CATCGCTTCA1680 ACAGGCATGG ACAGAAGCCT CAAGTTCTAC AGCCTGTAGG CCCTGGCCCT TCTGATGGAA1740 GCTGGGCCTC ATCTCAGTAG AGGGGTAGAA TTAGGGTTTG GGGGGGGGTG GGGGGAATCT1800 ATGGGGGGAG GGGGCTCTGT GGGGTGGGAC ATTCACATCA TTTCACTCTG GTCTGAGTGG1860 TGGCCTGAGA ACCATGGTGG CATGGACCAC CCTCATCCAT GCAACTCCAG GCCCCATGGG1920 AACGGATGTG GAAGGAAGAA CTGTCACCCT CTTAAGGCCC AGGGTCGGAG CCCAGGGCCT1980 CTCCCTTCCT GTCGTTCAAT GGACGTGGTG GTGGCTGTTC CACACCCATT TTGTTGCAGT2040 TCCTGTGAGA CAGGAGAGGC TGAGCCAAGG GAACTGTGAA GGGGATGGGC AGGAGGGCTT2100 GTGCAGGGTT TTGTAAGCAG TGATCTAGTT TCATTAAAAA AAGAAAACAA TAACCATAAC2160 CACCTCCCCG TGTCTGTCTG CACCAGGAGC ACCTGGGACT GGGAAGTCAA GGGGAGGGAG2220 CACACACTGG GACACTGGCT TCCGGGAAGC CCATCTTCCT TTCCTTTCAC AGCTCTTA

### (2) INFORMATION ON SEQ ID NO. 617:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 931 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

CAGGGGCGTG CAGCCCGCTT GCCAATCAGA GCGCGGCTGA GCGGCCCCGC AGCCAACCCC 60 CGAGGAGCGG CCGGCTGGCG TCCGCCGCGC CCAGGAGTTG GGGATGTCCT ACAAACCCAT120 CGCCCTGCT CCCAGCAGCA CCCCTGGCTC CAGCACCCCT GGGCCGGGCA CCCCGGTCCC180 TACAGGAAGC GTCCGTCGC CGTCGGGCTC AGTGCCAGGA GCCGGCGCTC CTTTCAGACC240 GCTGTTTAAC GACTTTGGAC CGCCTTCCAT GGGCTACGTG CAGGCGATGA AGCCACCCGG300 CGCCCAGGGC TCCCAGAGCA CCTACACGGA CCTGCTGTCA GTCATAGAGG AGATGGGCAA360 AGAGATCCGG CCTACCTATG CTGGCAGCAA GAGCGCCATG GAGCGCCTGA AGAGAGGTAT420 CATCCATGCC CGGGCCCTAG TCAGAGAGTG CCTGGCAGAG ACAGAGCGGA ACGCCCGCAC480 GTAACAGGAA GCGCCTCGGC CTCAGCGTCT GGACCTATCC GGCCACTGCA GAGCACCCGC540 TTCTCCCTGG CCTTCATCCC GAGTTGCACT AACCATCCTG GGCTTCCTGT CCTGTGTCCC600 TTGGTGGGTC CCCTCCAGGA ACCAAGGAGT GGCCCTCCAG GTGGCAGCAC TAAGGACACC660 CCCCCACAAC AAGAGTTAGC AGCGAGGTCC CCATGAGTCC CACCCATGAC CTGCCGACAG720 TGTTGCCCAC CGGAACTTTT GTGGCCCCTA CCGCTCAGCC CTTCCCAGCA CTTCTCCCAC780 TTTGTCCCGA GCCTCCTTCT CGCCCAGCAG GGGCACAGGC CTGGCACCTC CCTGCCTTGT840 GTCCTGAGCC ATAGTGACTC TTTTATCTGT GTGTCTTTTG CTAAATATGC CCTTTTTATA900 TTAATAAAAG ATGATTTGGA GTTGTGCTCT C

- (2) INFORMATION ON SEQ ID NO. 618:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 447 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

ELPSSPPPGL PEVAPDATST GLPDTPAAPE TSTNYPVECT EGSAGPQSLP LPILEPVKNP 60
CSVKDQTPLQ LSVEDTTSPN TKPCPPTPTT PETWGGGGG APSSTPCSAH LTPSSLFPSS120
LESSSEQKFY NFVILHARAD EHIALRVREK LEALGVPDGA TFCEDFQVPG RGELSCLQDA180
IDHSAFIILL LTSNFDCRLS LHQVNQAMMS NLTRQGSPDC VIPFLPLESS PAQLSSDTAS240
LLSGLVRLDE HSQIFARKVA NTFKPHRLQA RKAMWRKEQD TRALREQSQH LDGERMQAAA300
LNAAYSAYLQ SYLSYQAQME QLQVAFGSHM SFGTGAPYGV RMPFGGQGPL GAPPPFPTWP360
GCPQPPPLHA WQAGTPPPPS PQPAAFPQSL PFPQSPAFPT ASPAPPQSPG LQPLIIHHAQ420
MVQLGLNNHM WNQRGSQAPE DKTQEAE

- (2) INFORMATION ON SEQ ID NO. 619:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 205 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

ADAGGGTERS LLSLPPELLV LPGTDGAAPG GFWEPHVIWD WGALWGQNAL WGPGAPGSPA 60 TLSHLAGVPA AATPARMAGW HPPTALPTAS SLSTVTALPA VPSLPYGLTR TPSEPRAATP120 HYPPRTDGTA GAEQPHVEPE RVPGARGQDA GGRMTACPCL TTWGTPLDPG IGQDPIEHPG180 LPCALWTVED EVICHFQDIV REPFI 205

- (2) INFORMATION ON SEQ ID NO. 620:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 409 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

KSRLSVTLMP VQLSEHPEWN ESMHSLRISV GGLPVLASMT KAADPRFRPR WKVILTFFVG 60
AAILWLLCSH RPAPGRPPTH NAHNWRLGQA PANWYNDTYP LSPPQRTPAG IRYRIAVIAD120
LDTEPTAQDE NTWRSDLKKG YLTLSDSGDK VAVEWDKDHG VLESHLAEKG RGMELSDLIV180
FNGKLYSVDD RTGVVYQIEG SKAVPWVILS DGDGTVEKGF KAEWLAVKDE RLYVGGLGKE240
WTTTTGDVVN ENPEWVKVVG YKGSVDHENW VSNYNALRAA AGIQPPANLI HESACWSDTL300
QRWFFLPRRA SQERYSEKDD ERKGANLLLS ASPDFGDIAV SHVGAVVPTH GFSSFKFIPN360
TDDQIIVALK SEEDSGRVAS YIMAFTLDGR FLLPETKIGS VKYEGIEFI 409

- (2) INFORMATION ON SEQ ID NO. 621:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 249 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

KLSPDGLAQC FRFELNELDA FVFHASDLGL RQQEAPVQRE GHDVGGDSAA VLLGFEGHND 60 LVVGVGDELE GREAVSGDHR PDVAHSDVAE VRGGAQQQVG ALALVVLLAV ALLAGAARQE120 EPALQRVTPA GRLMDEVSWR LDAGSSPQGV VVGHPVLVVH AALVAHHLHP LRVLVHHITR180 SGRPLLAQAA HVQTLVLHCQ PFGLEAFLHG AVAVGQNHPG HGFAAFDLVD DPRPVIHGVE240 FPIENNQVG 249

- (2) INFORMATION ON SEQ ID NO. 622:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 255 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

AAAPVSLHDA AGDLRRDPGG GGGGGVPHGG GEGQEVVPAE PGVPAPQHAE PVAAAGAAQQ 60 LQTEEQPGLQ RLRLGPVRGA ARGGDARVRG PRGDRRVNPE SARALLPGDP QGPGTAAPRA120 LGLPPRCEPV GAPLAALALA RERRERGRFP RPCKCLFFNS SQCELCCECV RGGAPALSRR180

RVATPCPCPM VCNSDFAHRS TVPPSAHPFT LTPTLSLNTF IIVRRGRWDF GRSAAATASG240 GLIFIFALRW LKAFI 255

- (2) INFORMATION ON SEQ ID NO. 623:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 196 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

INAFSHRNAK ININPPDAVA AALRPKSQRP RLTIIKVFSE SVGVSVNGCA LGGTVERCAK 60 SELQTIGQGH GVATRRRLSA GAPPRTHSQQ SSHWEELKNK HLQGRGKRPR SRRSRARASA120 ARGAPTGSQR GGSPSARGAA VPGPCGSPGS RARALSGFTR RSPRGPRTRA SPPRAAPLTG180 PSRSRWSPGC SSVCSC

- (2) INFORMATION ON SEQ ID NO. 624:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 242 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

VESHRRAHTH TTVRSPETAR GWKPWPHRLS RYVHSPGRQP HGHGQHLCFC SGRRAFGGHP 60 RQGARASLLA LGLENSPGGS SPEERLGRLA VAGPPRGAQN VSQAGPEAEA PPLRFGHAWG120 AQTPRLGAPG PWTPLPTLPS HIPPFWSQTP AQRKEGFTEE GQGRAWPQGG DEDISGPGSC180 RLLWEEEPCV CKLLGLAARP TAGPSLDPCT WPSSCPLAAP GLGTGIEPRG LGWLGQGRDR240 EG 242

- (2) INFORMATION ON SEQ ID NO. 625:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 216 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

GLVMPGELRR PGLGPQAHGL PSPLCPPIFP LFGPRHQHKE RRGSQRKARA EPGPREGMRT 60 FPVQVAAGCS GRKSHASVNC WGWRPAPLQG PALTPARGHP AALWLPLALA QASSLEGWAG120 WARAGTGRGS TSDPDVGWLC PPRREAQQTS YTKAKSTIGE PRSHFMGRRP RPQGPQSKAR180 GRFIPEDSPP GAAPAWGGVS RPLGCLSVCG TPWSTP 216

- (2) INFORMATION ON SEQ ID NO. 626:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 299 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

PGISVSVDKM ESSPFNRRQW TSLSLRVTAK ELSLVNKNKS SAIVEIFSKY QKAAEETNME 60 KKRSNTENLS QHFRKGTLTV LKKKWENPGL GAESHTDSLR NSSTEIRHRA DHPPAEVTSH120 AASGAKADQE EQIHPRSRLR SPPEALVQGR YPHIKDGEDL KDHSTESKKM ENCLGESRHE180 VEKSEISENT DASGKIEKYN VPLNRLKMMF EKGEPTQTKI LRAQSRSASG RKISENSYSL240 DDLEIGPGQL SSSTFDSEKN ESRRNLELPR LSETSIKDRM AKYQAAVSKQ SSSPTIPMS 299

- (2) INFORMATION ON SEQ ID NO. 627:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 94 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

DSAPSPGFSH FFFNTVRVPF LKCWERFSVL LLFFSMFVSS AAFWYLENIS TIADDLFLLT60 RESSLAVTLN DSEVHCRLLN GDDSILSTDT EIPG 94

- (2) INFORMATION ON SEQ ID NO. 628:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 765 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

IRPVVQLTAI EILAWGLRNM KNFQMASITS PSLVVECGGE RVESVVIKNL KKTPNFPSSV 60
LFMKVFLPKE ELYMPPLVIK VIDHRQFGRK PVVGQCTIER LDRFRCDPYA GKEDIVPQLK120
ASLLSAPPCR DIVIEMEDTK PLLASKLTEK EEEIVDWWSK FDASSGEHEK CGQYIQKGYS180
KLKIYNCELE NVAEFEGLTD FSDTFKLYRG KSDENEDPSV VGEFKGSFRI YPLPDDPSVP240
APPRQFRELP DSVPQECTVR IYIVRGLELQ PQDNNGLCDP YIKITLGKKV IEDRDHYIPN300
EEYCVSGVNT WRDQLRPTQL LQNVARFKGF PQPILSEDGS RIRYGGRDYS LDEFEANKIL420
HQHLGAPEER LALHILRTQG LVPEHVETRT LHSTFQPNIS QGKLQMWVDV FPKSLGPPGP480
PFNITPRKAK KYYLRVIIWN TKDVILDEKS ITGEEMSDIY VKGWIPGNEE NKQKTDVHYRS40
SLDGEGNFNW RFVFPFDYLP AEQLCIVAKK EHFWSIDQTE FRIPPRLIIQ IWDNDKFSLD600
DYLGFLELDL RHTIIPAKSP EKCRLDMIPD LKAMNPLKAK TASLFEQKSM KGWWPCYAEK660
DGARVMAGKV VIIGLLFLLI LLLFVAVLLY SLPNYLSMKI VKPNV 765

# (2) INFORMATION ON SEQ ID NO. 629:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 289 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

ETQVVIQRKL VIVPYLNDQP GWDSKFRLVN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60 FTIQRSVMDI CFLFVFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVPDDH TQVVFLGFPG120 CDVERRAWWP QTLGENIHPH LKFSLGNVGL EGAVQSPCFH VLRDQPLSPE DVKSKPLFRG180 PEVLVQDFVG FKFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISPGIDSR240 NTVLLWYAAV GPKAGKESVF QINNCFSYFF IPGKGVIIID RNFQVFFLR 289

#### (2) INFORMATION ON SEQ ID NO. 630:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 824 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

RVSVLAAASS ALPVAPREAG VTNWPAGCVP EVRSTGEKEV AKTLHRRSRP EWCGARDPPA 60 MLLFVLTCLL AVFPAISTKS PIFGPEEVNS VEGNSVSITC YYPPTSVNRH TRKYWCRQGA120 RGGCITLISS EGYVSSKYAG RANLTNFPEN GTFVVNIAQL SQDDSGRYKC GLGINSRGLS180 FDVSLEVSQG PGLLNDTKVY TVDLGRTVTI NCPFKTENAQ KRKSLYKQIG LYPVLVIDSS240 GYVNPNYTGR IRLDIQGTGQ RLFSVVINQL RLSDAGGYLC QAGDDSNSNK KNADLQVLKP300 EPELVYEDLR GSVTFHCALG PEVANVAKFL CRQSSGENCD VVVNTLGKRA PAFEGRILLN360 PQDKDGSFSV VITGLRKEDA GRYLCGAHSD GQLQEGSPIQ AWQLFVNEES TIPRSPTVVK420 GVAGGSVAVL CPYNRKESKS IKYWCLWEGA QNGRCPLLVD SEGWVKAQYE GRLSLLEEPG480 NGTFTVILNQ LTSRDAGFYW CLTNGDTLWR TTVEIKIEG EPNLKVPGNV TAVLGETLKV540 PCHFPCKFSS YEKYWCKWNN TGCQALPSQD EGPSKAFVNC DENSRLVSLT LNLVTRADEG600 WYWCGVKQGH FYGETAAVYV AVEERKAAGS RDVSLAKADA APDEKVLDSG FREIENKAIQ660 DPRLFAEEKA VADTRDQADG SRASVDSGSS EEQGGSSRAL VSTLVPLGLV LAVGAVAVGV720 ARARHKNVD RVSIRSYRTD ISMSDFENSR EFGANDNMGA SSITQETSLG GKEEFVATTE780 STTETKEPKK AKRSSKEEAE MAYKDFLLQS STVAAEAQDG PQEA

- (2) INFORMATION ON SEQ ID NO. 631:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 267 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

ADIAGPRCLP LFNCHIDGCS LSIEVALLHS TPVPALISPG HQVQGQGDKP AVLVTVHEGL 60
AGAFVLAGQG LAARVIPLAP VFLVRGEFAW KVTGDLESLS QHSRDIPWYL EVWFSFDNLD120
LHGGPPESIA VGQTPVEAGV PAGELVEDDS EGAVAWLLQQ GEAALVLGLN PPLAVHQQGA180
AAILGPFPET PVLDAFAFLT VVGAEHGHRA SCHPLHHSGA AGNRGLLIDE ELPGLDRRAF240
LQLTIRMGST QVAPCILLPQ ACDHTE

- (2) INFORMATION ON SEQ ID NO. 632:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 140 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

GETRVHSQQG GGIKAPSWDW FFREPGPLVK GLLGHVKQYL EQPRPWGYQV ERREGRRLPC 60 THLPWWAGFS LLGSTLPPSV HDTDPRASPC PRPSYRLLFQ DITDNPERME KGGAWVPAVS120 GQKEVACGNL RSPHPRFPKR 140

- (2) INFORMATION ON SEQ ID NO. 633:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

  VFPCHLVGAG PTPATTSGTA KGSTRCDYPG PCWQLRIPGT CSDPVSGSSE SQEPRMRALC 60

  SPSSKTQGSP PRKGAHVPQR GWLPGCYLFY PTSAAESQGE TASHPKPLGF SREKNLSQKH120
  DLFSGCK 127
  - (2) INFORMATION ON SEQ ID NO. 634:
    - (i) SEQUENCE CHARACTERISTIC:
      - (A) LENGTH: 140 amino acids
      - (B) TYPE: Protein
      - (C) STRAND: individual
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: ORF
    - (iii) HYPOTHETICAL: yes
    - (vi) ORIGIN
      - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

HHQKHMQGKG SYWASGLLSP WLGRKGREDG WGSLFGIDDV HEFGLEGSTT HKEAIHIRLA 60 GQLLAGCPSH RASINDTGAL SHRIRDVGLQ PSSELLVYFL GLLGCCSLAS TNGPHRLIGQ120 DDLAPVLHVI CDDLLVWWEG 140

- (2) INFORMATION ON SEQ ID NO. 635:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 101 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

KVIADNVKDW SKVVLAYEPV WAIGTGKTAT PQQAQEVHEK LRGWLKSNVS DAVAQSTRII 60 YGGSVTGATC KELASQPDVD GFLVGGASLK PEFVDIINAK Q 101

- (2) INFORMATION ON SEQ ID NO. 636:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 329 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

DSIFPLWAVL ALSPPGIRVR MKKSSVSGMT AAGWVVWGEA EGKAALRLGV EFLEVWGGGR 60 VFNLEKSQPA RAERECERGS SEGARNGVGG SGGRSVAVAL VHQHGVRLLG DLQQRVHVGA120 APAPQVAGLP PLRAALVVVG AHLHHLGGLE HFHLALADLL DVEGEGWHLV DRGLGARVHH180 VVGREGFAQL VPRRLQFLAP LGGHQARAQL VHALLQGVPR LLQVFLGLEA RLLQVLAGTH240 LGLLHLLLGE GLLEVVHAPQ ALRLIRSARD SSITSSTSTA SSDESSAAA SSSGRSPSPS300 SSPSFSGSAS DSFSDLLMLS LAGSFTSSW 329

(2	) INFORMATION	ОИ	SEQ	ID	NO.	637:
----	---------------	----	-----	----	-----	------

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 263 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

GRLPGYPDRR GPGASSAGAQ AAEEPSGAGS EELIKSDQVN GVLVLSLLDK IIGAVDQIQL 60 TQAQLEERQA EMEGAVQSIQ GELSKLGKAH ATTSNTVSKL LEKVRKVSVN VKTVRGSLER120 QAGQIKKLEV NEAELLRRN FKVMIYQDEV KLPAKLSISK SLKESEALPE KEGEELGEGE180 RPEEDAAALE LSSDEAVEVE EVIEESRAER IKRRACGAWT TSRRPSPRRR WRRPRCVPAR240 TWRRRASRPR KTWRRRGTPW RSA

- (2) INFORMATION ON SEQ ID NO. 638:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 205 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

SGDLRLLVDT SKVQEAWVPS QDTHHTQELL AVQGSLVSGY RPGGGFGAAP VHEDPHLLGP 60
ASRGAPETAA FFFFFFFFP EQHLRVGLLL LPPRLSPRPG PAWPVPNPVG WPGHLHQGGQ 120
LLAGTNKPFH LAMVVVFSMD RGPETRAGRG REHTSLGVGT SLXTPQQLXG PRXXFPXAVQ 180
ASPXPGVCSL AWVELCHIXD KQXGG 205

- (2) INFORMATION ON SEQ ID NO. 639:
  - (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 171 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

PVTPRDXPGA GGGSXEGPMQ HPGQSRPXPL AXPAPXWXLM APCGALTCWA RLXLGLSAPX 60 LLIXDVTELD PSQAAHSWTW ASLHCXGKXX PRAXKLLRGX EAGAHPQASV FSAPPCPRFR120 ASVHREHHHH GQVEGFISPC QQLSSLVQVA WPAHWIGDGP GWARSGAQSG R 171

- (2) INFORMATION ON SEQ ID NO. 640:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 161 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

ISRNEGVLVR GPKSPRSLLR SHSEPPALVL WRDHRLVPGT DYCKDTALVP TEKNTGQQEH 60 TFSQYLATPH SELTITHGKW VHSSLWSDPA GLGRQEQHSS SSLSPRQRES LNCKRSGAYT120 VREKEKGGRK GFSPRPPRDA HREGGKEREK SVLESEATLS K

- (2) INFORMATION ON SEQ ID NO. 641:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 127 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

CAYRTEKWKS HTVPCSPEVK LVLTLALRAF SSMEPLGLGR KARVSAHRHT SYLQDIDCLC 60 RGSTGQPTAN TAASLVSASL LPVHPGDYSW INLPKNSAFI MSLFCSKTQN GSLPPRGRPS120 HHCIPNR

- (2) INFORMATION ON SEQ ID NO. 642:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 136 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

WGXGRVRVXG WXRKPMKXGI PPEXHGPITA DGHRXLXXLP PXGXRCXXAD PKGXGLXALF 60 XKXPPXEXCL LSXXPXXPVT HRAGMEFNGX FWXXTLVHGQ TSLLXGYXTR LKXKIVCCHS120 SGXWSVCGLH RFHRNQ

- (2) INFORMATION ON SEQ ID NO. 643:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 132 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

GRXSRAWGLG CPSLLSPISL RLPVPPPRPP NLRPPATPGA PTXPXQNTAX LKXLLELSXX 60 LSGLGLMGXR AGTCTWVAXE AHEDXDTPRV PWTXYXRWSS XPXAIATXGX SLXXGRPQRE120 XPXRVVXKXT TX

- (2) INFORMATION ON SEQ ID NO. 644:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 131 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

GVETTANSST SLRSTTLEKE VPVIFIHPLN TGLFRIKIQG ATGKFNMVIP LVDGMIVSRR 60 ALGFLVRQTV INICRRKRLE SDSYSPPMSA GNRKSPTLST STGTSSWSQS FILHFSRRLD120 SRTAVLRPLN F

- (2) INFORMATION ON SEQ ID NO. 645:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 86 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

LTNMSDHLFG WLLLEMAVVM FSGLCQPTDP CQVLEILLLP RCYFSAGIKL LXVARPRTSK60 DSCYSATVYT AHLSYSHVLS SLVRLF 86

- (2) INFORMATION ON SEQ ID NO. 646:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 96 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

KAPNPSVLHT VRMQLIADRC CELYICKRCF TTSAGFITAS WSRVAILPAI PAKQTPENYP60 LRSGVLRKFL EPKIRRNPGL SFLRSKMYYQ LRPGEH

- (2) INFORMATION ON SEQ ID NO. 647:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 92 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

SSACRCTTRS TGQQSAASGR CGGPRGWGPS TGATPRQLTM NIPFQSIHFI TYEFLQEQVN60 PHRTYNPQSH IISGGLAGAL AAAARGPLDV LR 92

- (2) INFORMATION ON SEQ ID NO. 648:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 280 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

AVGSAALFKD GGGGTSAAEA GAAGQRLRSV NCLAYDEAIM AQQDRIQQEI AVQNPLVSER 60 LELSVLYKEY AEDDNIYQQK IKDLHKKYSY IRKTRPDGNC FYRAFGFSHL EALLDDSKEL120 QRFKAVSAKS KEDLVSQGFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL180 VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEPM CKESDHIHII ALAQALSVS1240 QVEYMDRGEG GTTNPHIFPE GSEPKVYLLY RPGHYDILYK

- (2) INFORMATION ON SEQ ID NO. 649:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 244 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

DHLQPQKNLC TCLAPGRGGQ QGSSGLEPAL FVEDIVVSRP VEKVDLGLGA LREDVRIGGA 60
ALAAVHVLHL DGHAEGLGQR NDVDVVALLA HGLHLLLAEL LDSPSTLDEV LEELALALQV120
ARGEQPQVDH KVVGGALVIE GGQQVGDRGL LLHLLNQVHE RVVEILNCEF SEALGHQVFL180
ALGRHSLEPL QLLAVIQQCL QVGESESPIE TVAVRPGLAD VRVLFVEVLD LLLIDVVIFS240
ILLV 244

- (2) INFORMATION ON SEQ ID NO. 650:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 424 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

LTTTCVSSSA PSKTSLIMNP HASTNGQLSV HTPKRESLSH EEHPHSHPLY GHGVCKWPGC 60
EAVCEDFQSF LKHLNSEHAL DDRSTAQCRV QMQVVQQLEL QLAKDKERLQ AMMTHLHVKS120
TEPKAAPQPL NLVSSVTLSK SASEASPQSL PHTPTTPTAP LTPVTQGPSV ITTTSMHTVG180
PIRRRYSDKY NVPISSADIA QNQEFYKNAE VRPPFTYASL IRQAILESPE KQLTLNEIYN240
WFTRMFAYFR RNAATWKNAV RHNLSLHKCF VRVENVKGAV WTVDEVEFQK RRPQKISGNP300
SLIKNMQSSH AYCTPLNAAL QASMAENSIP LYTTASMGNP TLGNLASAIR EELNGAMEHT360
NSNESDSSPG RSPMQAVHPV HVKEEPLDPE EAEGPLSLVT TANHSPDFDH DRDYEDEPVN420
EDME

- (2) INFORMATION ON SEQ ID NO. 651:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

STNAGCTAVR ATACKRQRAP ASHDDPPACE VYRTQSRPSA LESGIKCHSL QVRIGGFSTE 60 LTSYSNDPNR PPDSRHPRPL CHHNHQHAHG GTHPQAVLRQ IQRAHFVSRY CAEPRIL 117

- (2) INFORMATION ON SEQ ID NO. 652:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 426 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEO ID NO: 652:

PEAGLESCSE QSDFPEHIFI MIHTNLKKKF SCCVLVFLLF AVICVWKEKK KGSYYDSFKL 60

QTKEFQVLKS LGKLAMGSDS QSVSSSSTQD PHRGRQTLGS LRGLAKAKPE ASFQVWNKDS120 SSKNLIPRLQ KIWKNYLSMN KYKVSYKGPG PGIKFSAEAL RCHLRDHVNV SMVEVTDFPF180 NTSEWEGYLP KESIRTKAGP WGRCAVVSSA GSLKSSQLGR EIDDHDAVLR FNGAPTANFQ240 QDVGTKTTIR LMNSQLVTTE KRFLKDSLYN EGILIVWDPS VYHSDIPKWY QNPDYNFFNN300 YKTYRKLHPN QPFYILKPQM PWELWDILQE ISPEEIQPNP PSSGMLGIII MMTLCDQVDI360 YESLPSKRKT DVCYYYQKFF DSACTMGAYH PLLYEKNLVK HLNQGTDEDI YLLGKATLPG420 FRTIHC

- (2) INFORMATION ON SEQ ID NO. 653:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 139 amino acids
    - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

RCVQGSHFVL SRKTSLLIAN PPGAAGPSGP QELALLSMGG KVYWVCRPRP IFLRMIKTHL 60 CWFMVTCAAG FGDAEVCRSI SGGLDAVLPF SLWCWLCGLC GTFCPLARCT LGRGGCGCSA120 RSVAAARSAP TPVGIGSLC 139

- (2) INFORMATION ON SEQ ID NO. 654:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 243 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

WRQLARGWGA LSRASCPALP RLANNTVRMA KGDPKKPKGK MSAYAFFVQT CREEHKKKNP 60
EVPVNFAEFS KKCSERWKTM SGKEKSKFDE MAKADKVRYD REMKDYGPAK GGKKKKDPNA120
PKRPPSGFFL FCSEFRPKIK STNPGISIGD VAKKLGEMWN NLNDSEKQPY ITKTAKLKEK180
YEKDVADYKS KGKFDGAKGP AKVARKKVEE EDEEDGGGGG GGGGGTYSRV GWWSSPKEGE240

- (2) INFORMATION ON SEQ ID NO. 655:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 110 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

TEQEESRRWP FGSIRILLL ASLSWSIILH FPIIAHFICL CHFIKFRFLF PGHRLPPLRA 60 LLGKFRKIDR DLWVFLLMFF SACLHKEGIS GHLALWFLGV TFSHPDCIVR 110

#### (2) INFORMATION ON SEQ ID NO. 656:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 356 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

VGCSHAAQLH SAPELQTTRQ ELSHALYQHD AACRVIARLT KEVTAAREAL ATLKPQAGLI 60
VPQAVPSSQP SVVGAGEPMD LGELVGMTPE IIQKLQDKAT VLTTERKKRG KTVPEELVKP120
EELSKYRQVA SHVGLHSASI PGILALDLCP SDTNKILTGG ADKNVVVFDK SSEQILATLK180
GHTKKVTSVV FHPSQDLVFS ASPDATIRIW SVPNASCVQV VRAHESAVTG LSLHATGDYL240
LSSSDDQYWA FSDIQTGRVL TKVTDETSGC SLTCAQFHPD GLIFGTGTMD SQIKIWDLKE300
RTNVANFPGH SGPITSIAFS ENGYYLATAA DDSSVKLWDL RKLRTLRLCS WITTLR 356

### (2) INFORMATION ON SEQ ID NO. 657:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 240 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

LAQIPELDRG VISRCSQVVT ILREGDASDG ARVAREVGHI STFLQVPDLD LRVHGSCSKD 60 ESVRVELCTG ERAAGGLICH LGEHTPCLDV RESPVLIIGG AQEIVASGMK AEACHSTLMG120 PNHLYTRGIG DRPNPDSGIG GSRKHQVLGR VKHHAGDLLG MAFEGSQDLF RTFVKHNDIF180 IRPTSEDLVG VGRAEVQGQD PRNAGTVQPH VGCHLPVFAE LFWLHQLLRH SLPSLLALRG240

# (2) INFORMATION ON SEQ ID NO. 658:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 162 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:

EHNSKSSFIN IKRAYLAKDT QIKESLWLRT QGREVPGLCP CWARRLGTK WEKCWEGLSG 60 RGHKSSGGQH CRQVMGGTHG DLAANSCCGG VSLVLPPGGP LLGSWRGPTK GHRTGSPGWL120 VQLGMKAREK RVLCSGRIGP DAEAEALPVT CGRSALSLPG TL 162

- (2) INFORMATION ON SEQ ID NO. 659:
  - (i) SEQUENCE CHARACTERISTIC:
    - (A) LENGTH: 148 amino acids
    - (B) TYPE: Protein
    - (C) STRAND: individual
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: ORF
  - (iii) HYPOTHETICAL: yes
  - (vi) ORIGIN
    - (A) ORGANISM: HUMAN
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:

RLWTAFHGLR AGDEATRRPG LPEHLHGPAV SHRGDGQRDP AYLCWQQERH GAPEERYHPC 60 PGPSQRVPGR DRAERPHVTG SASASASGPI RPLQSTRFSL AFIPSCTNHP GLPVLCPLVG120 PLQEPRSGPP GGSTKDTPPQ QELAARSP